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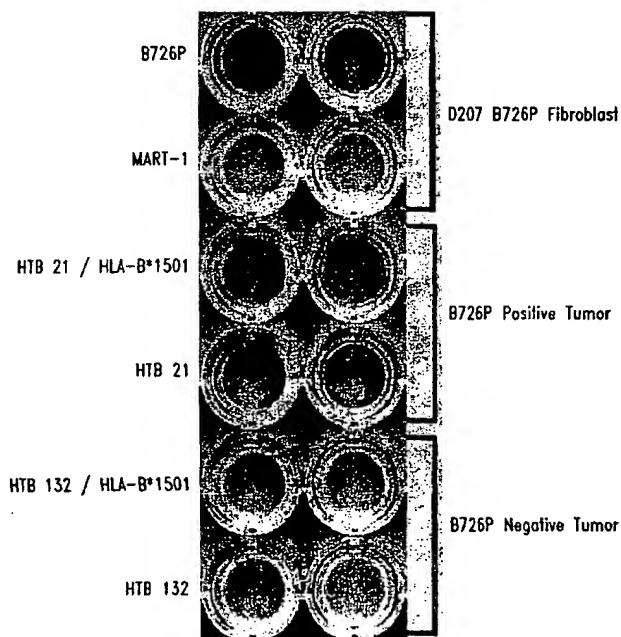
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(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF BREAST CANCER

D207 B726P-specific CTL Clone 1-9A recognize HTB 21  
a breast tumor cell line that expresses HLA-B\*1501 and B726P



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer, are disclosed. Illustrative compositions comprise one or more breast tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly breast cancer.



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## COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF BREAST CANCER

### TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of  
5 cancer, such as breast cancer. The invention is more specifically related to  
polypeptides, comprising at least a portion of a breast tumor protein, and to  
polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides  
are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for  
the diagnosis and treatment of breast cancer.

10

### BACKGROUND OF THE INVENTION

#### Field of the Invention

Breast cancer is a significant health problem for women in the United  
States and throughout the world. Although advances have been made in detection and  
15 treatment of the disease, breast cancer remains the second leading cause of cancer-  
related deaths in women, affecting more than 180,000 women in the United States each  
year. For women in North America, the life-time odds of getting breast cancer are one  
in eight.

#### Description of the Related Art

20

No vaccine or other universally successful method for the prevention or  
treatment of breast cancer is currently available. Management of the disease currently  
relies on a combination of early diagnosis (through routine breast screening procedures)  
and aggressive treatment, which may include one or more of a variety of treatments  
such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of  
25 treatment for a particular breast cancer is often selected based on a variety of prognostic  
parameters, including an analysis of specific tumor markers. *See, e.g.*, Porter-Jordan  
and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers  
often leads to a result that is difficult to interpret, and the high mortality observed in  
breast cancer patients indicates that improvements are needed in the treatment,  
30 diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for the treatment and diagnosis of breast cancer. The present invention fulfills these needs and further provides other related advantages.

#### SUMMARY OF THE INVENTION

5           In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

10           (b) complements of the sequences provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

15           (d) sequences that hybridize to a sequence provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, under moderately stringent conditions;

20           (e) sequences having at least 75% identity to a sequence of SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576; and

25           (g) degenerate variants of a sequence provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%,

30

and most preferably in at least about 50% of breast tumors samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for normal tissues.

The present invention, in another aspect, provides polypeptide  
5 compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO:62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-  
10 503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627.

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

15 The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID  
20 NO: 62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627 or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576.

25 The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a  
30 physiologically acceptable carrier.

Within a related aspect of the present invention, the pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant.

5           The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

10           Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

15           Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

20           The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating the expression, purification and/or immunogenicity of the polypeptide(s).

25           The present invention further provides, in other aspects, fusion proteins that

comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins. Exemplary fusion proteins according to the present invention comprise a first amino acid portion and a second amino acid portion wherein  
30   the first amino acid portion includes 9 or more contiguous amino acids from mammaglobin as depicted by amino acids 1-93 of SEQ ID NO:493 (SEQ ID NO:503);

wherein the second amino acid portion includes 9 or more contiguous amino acids from B726P as depicted by SEQ ID NO:475, SEQ ID NO:469, or SEQ ID NO:176; and wherein the first amino acid portion is connected to either the amino terminal or carboxy-terminal end of the second amino acid portion.

5 Still further embodiments of the present invention provide fusion proteins

wherein said first amino acid portion is selected from the group consisting of: IDELKECFLNQTDETLSNVE (SEQ ID NO:496; amino acids 59-78 of SEQ ID NO:493); TTNAIDELKECFLNQ (SEQ ID NO:497; amino acids 55-69 of SEQ ID NO:493); SQHCYAGSGCPLLENVISKTI (SEQ ID NO:498; amino acids 13-33 of  
10 SEQ ID NO:493); EYKELLQEFIDDNATTNAID (SEQ ID NO:499; amino acids 41-60 of SEQ ID NO:493); KLLMVLMLA (SEQ ID NO:500; amino acids 2-10 of SEQ ID NO:493); QEFIDDNATTNAI (SEQ ID NO:501; amino acids 47-59 of SEQ ID NO:493); LKECFLNQTDETL (SEQ ID NO:502; amino acids 62-74 of SEQ ID  
15 NO:493), and any one of the amino acid sequences set forth in SEQ ID NO:578-593.

Alternative embodiments provide fusion proteins wherein the second amino acid portion includes 9 or more contiguous amino acids encoded by (1) the combined upstream and downstream open reading frame (ORF) of B726P as depicted in SEQ ID NO:475; (2) the upstream ORF of B726P as depicted in SEQ ID NO:469; and  
20 (3) the downstream ORF of B726P as depicted in SEQ ID NO:176. Fusion proteins according to the present invention may also comprise a second amino acid portion that includes 9 or more contiguous amino acids from the amino acid sequence depicted by amino acids 1-129 of SEQ ID NO:475. Still additional exemplary fusion proteins are depicted herein by SEQ ID NO:493, SEQ ID NO:494, and SEQ ID NO:495.

25 Fusion proteins are provided wherein the mammaglobin amino acid portion is connected to the amino-terminus of the B726P amino acid portion while other fusion proteins are provided wherein the mammaglobin amino acid portion is connected to the carboxy-terminus of the B726P amino acid portion. The connection between the mammaglobin amino acid portion and the B726P portion may be a covalent bond.  
30 Additionally, a stretch of amino acids either unrelated or related to either mammaglobin

and/or B726P may be incorporated between or either amino- or carboxy-terminal to either the mammaglobin and/or B726P amino acid portion.

The present invention also provides isolated polynucleotides that encode any of the fusion proteins that are specifically disclosed herein as well as those fusion  
5 proteins that may be accomplished with routine experimentation by the ordinarily skilled artisan.

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The  
10 patient may be afflicted with breast cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a  
15 patient a pharmaceutical composition as recited above. The patient may be afflicted with breast cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological  
20 sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological  
25 sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that  
30 expresses such a polypeptide; under conditions and for a time sufficient to permit the

stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a  
5 patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a  
10 polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

15 Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a breast cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of  
20 polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps  
25 of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount  
30 detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) 5 detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one 10 oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

15 In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) 20 using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as 25 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All 30 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

## BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Fig. 1 shows the results of a Northern blot of the clone SYN18C6 (SEQ ID NO:40).

Fig. 2 shows the results of an IFN-gamma ELISPOT assay demonstrating  
5 that the B726P-specific CTL clone recognizes and lyses breast tumor cell lines  
expressing B726P.

SEQ ID NO:1 is the determined cDNA sequence of JBT2.  
SEQ ID NO:2 is the determined cDNA sequence of JBT6.  
SEQ ID NO:3 is the determined cDNA sequence of JBT7.  
10 SEQ ID NO:4 is the determined cDNA sequence of JBT10.  
SEQ ID NO:5 is the determined cDNA sequence of JBT13.  
SEQ ID NO:6 is the determined cDNA sequence of JBT14.  
SEQ ID NO:7 is the determined cDNA sequence of JBT15.  
SEQ ID NO:8 is the determined cDNA sequence of JBT16.  
15 SEQ ID NO:9 is the determined cDNA sequence of JBT17.  
SEQ ID NO:10 is the determined cDNA sequence of JBT22.  
SEQ ID NO:11 is the determined cDNA sequence of JBT25.  
SEQ ID NO:12 is the determined cDNA sequence of JBT28.  
SEQ ID NO:13 is the determined cDNA sequence of JBT32.  
20 SEQ ID NO:14 is the determined cDNA sequence of JBT33.  
SEQ ID NO:15 is the determined cDNA sequence of JBT34.  
SEQ ID NO:16 is the determined cDNA sequence of JBT36.  
SEQ ID NO:17 is the determined cDNA sequence of JBT37.  
SEQ ID NO:18 is the determined cDNA sequence of JBT51.  
25 SEQ ID NO:19 is the determined cDNA sequence of JBTT1.  
SEQ ID NO:20 is the determined cDNA sequence of JBTT7.  
SEQ ID NO:21 is the determined cDNA sequence of JBTT11.  
SEQ ID NO:22 is the determined cDNA sequence of JBTT14.  
SEQ ID NO:23 is the determined cDNA sequence of JBTT18.  
30 SEQ ID NO:24 is the determined cDNA sequence of JBTT19.  
SEQ ID NO:25 is the determined cDNA sequence of JBTT20.

- SEQ ID NO:26 is the determined cDNA sequence of JBTT21.  
SEQ ID NO:27 is the determined cDNA sequence of JBTT22.  
SEQ ID NO:28 is the determined cDNA sequence of JBTT28.  
SEQ ID NO:29 is the determined cDNA sequence of JBTT29.  
5 SEQ ID NO:30 is the determined cDNA sequence of JBTT33.  
SEQ ID NO:31 is the determined cDNA sequence of JBTT37.  
SEQ ID NO:32 is the determined cDNA sequence of JBTT38.  
SEQ ID NO:33 is the determined cDNA sequence of JBTT47.  
SEQ ID NO:34 is the determined cDNA sequence of JBTT48.  
10 SEQ ID NO:35 is the determined cDNA sequence of JBTT50.  
SEQ ID NO:36 is the determined cDNA sequence of JBTT51.  
SEQ ID NO:37 is the determined cDNA sequence of JBTT52.  
SEQ ID NO:38 is the determined cDNA sequence of JBTT54.  
SEQ ID NO:39 is the determined cDNA sequence of SYN17F4.  
15 SEQ ID NO:40 is the determined cDNA sequence of SYN18C6 (also  
known as B709P).  
SEQ ID NO:41 is the determined cDNA sequence of SYN19A2.  
SEQ ID NO:42 is the determined cDNA sequence of SYN19C8.  
SEQ ID NO:43 is the determined cDNA sequence of SYN20A12.  
20 SEQ ID NO:44 is the determined cDNA sequence of SYN20G6.  
SEQ ID NO:45 is the determined cDNA sequence of SYN20G6-2.  
SEQ ID NO:46 is the determined cDNA sequence of SYN21B9.  
SEQ ID NO:47 is the determined cDNA sequence of SYN21B9-2.  
SEQ ID NO:48 is the determined cDNA sequence of SYN21C10.  
25 SEQ ID NO:49 is the determined cDNA sequence of SYN21G10.  
SEQ ID NO:50 is the determined cDNA sequence of SYN21G10-2.  
SEQ ID NO:51 is the determined cDNA sequence of SYN21G11.  
SEQ ID NO:52 is the determined cDNA sequence of SYN21G11-2.  
SEQ ID NO:53 is the determined cDNA sequence of SYN21H8.  
30 SEQ ID NO:54 is the determined cDNA sequence of SYN22A10.  
SEQ ID NO:55 is the determined cDNA sequence of SYN22A10-2.

SEQ ID NO:56 is the determined cDNA sequence of SYN22A12.

SEQ ID NO:57 is the determined cDNA sequence of SYN22A2 (also referred to as B718P).

SEQ ID NO:58 is the determined cDNA sequence of SYN22B4.

5 SEQ ID NO:59 is the determined cDNA sequence of SYN22C2.

SEQ ID NO:60 is the determined cDNA sequence of SYN22E10.

SEQ ID NO:61 is the determined cDNA sequence of SYN22F2.

SEQ ID NO:62 is a predicted amino acid sequence for SYN18C6 (also known as B709P).

10 SEQ ID NO:63 is the determined cDNA sequence of B723P.

SEQ ID NO:64 is the determined cDNA sequence for B724P.

SEQ ID NO:65 is the determined cDNA sequence of B770P.

SEQ ID NO:66 is the determined cDNA sequence of B716P.

SEQ ID NO:67 is the determined cDNA sequence of B725P.

15 SEQ ID NO:68 is the determined cDNA sequence of B717P.

SEQ ID NO:69 is the determined cDNA sequence of B771P.

SEQ ID NO:70 is the determined cDNA sequence of B722P.

SEQ ID NO:71 is the determined cDNA sequence of B726P.

SEQ ID NO:72 is the determined cDNA sequence of B727P.

20 SEQ ID NO:73 is the determined cDNA sequence of B728P.

SEQ ID NO:74-87 are the determined cDNA sequences of isolated clones which show homology to known sequences.

SEQ ID NO:88 is the determined cDNA sequence of 13053.

SEQ ID NO:89 is the determined cDNA sequence of 13057.

25 SEQ ID NO:90 is the determined cDNA sequence of 13059.

SEQ ID NO:91 is the determined cDNA sequence of 13065.

SEQ ID NO:92 is the determined cDNA sequence of 13067.

SEQ ID NO:93 is the determined cDNA sequence of 13068.

SEQ ID NO:94 is the determined cDNA sequence of 13071.

30 SEQ ID NO:95 is the determined cDNA sequence of 13072.

SEQ ID NO:96 is the determined cDNA sequence of 13073.

SEQ ID NO:97 is the determined cDNA sequence of 13075.  
SEQ ID NO:98 is the determined cDNA sequence of 13078.  
SEQ ID NO:99 is the determined cDNA sequence of 13079.  
SEQ ID NO:100 is the determined cDNA sequence of 13081.  
5 SEQ ID NO:101 is the determined cDNA sequence of 13082.  
SEQ ID NO:102 is the determined cDNA sequence of 13092.  
SEQ ID NO:103 is the determined cDNA sequence of 13097.  
SEQ ID NO:104 is the determined cDNA sequence of 13101.  
SEQ ID NO:105 is the determined cDNA sequence of 13102.  
10 SEQ ID NO:106 is the determined cDNA sequence of 13119.  
SEQ ID NO:107 is the determined cDNA sequence of 13131.  
SEQ ID NO:108 is the determined cDNA sequence of 13133.  
SEQ ID NO:109 is the determined cDNA sequence of 13135.  
SEQ ID NO:110 is the determined cDNA sequence of 13139.  
15 SEQ ID NO:111 is the determined cDNA sequence of 13140.  
SEQ ID NO:112 is the determined cDNA sequence of 13146.  
SEQ ID NO:113 is the determined cDNA sequence of 13147.  
SEQ ID NO:114 is the determined cDNA sequence of 13148.  
SEQ ID NO:115 is the determined cDNA sequence of 13149.  
20 SEQ ID NO:116 is the determined cDNA sequence of 13151.  
SEQ ID NO:117 is the determined cDNA sequence of 13051  
SEQ ID NO:118 is the determined cDNA sequence of 13052  
SEQ ID NO:119 is the determined cDNA sequence of 13055  
SEQ ID NO:120 is the determined cDNA sequence of 13058  
25 SEQ ID NO:121 is the determined cDNA sequence of 13062  
SEQ ID NO:122 is the determined cDNA sequence of 13064  
SEQ ID NO:123 is the determined cDNA sequence of 13080  
SEQ ID NO:124 is the determined cDNA sequence of 13093  
SEQ ID NO:125 is the determined cDNA sequence of 13094  
30 SEQ ID NO:126 is the determined cDNA sequence of 13095  
SEQ ID NO:127 is the determined cDNA sequence of 13096  
SEQ ID NO:128 is the determined cDNA sequence of 13099

SEQ ID NO:129 is the determined cDNA sequence of 13100  
SEQ ID NO:130 is the determined cDNA sequence of 13103  
SEQ ID NO:131 is the determined cDNA sequence of 13106  
SEQ ID NO:132 is the determined cDNA sequence of 13107  
5 SEQ ID NO:133 is the determined cDNA sequence of 13108  
SEQ ID NO:134 is the determined cDNA sequence of 13121  
SEQ ID NO:135 is the determined cDNA sequence of 13126  
SEQ ID NO:136 is the determined cDNA sequence of 13129  
SEQ ID NO:137 is the determined cDNA sequence of 13130  
10 SEQ ID NO:138 is the determined cDNA sequence of 13134  
SEQ ID NO:139 is the determined cDNA sequence of 13141  
SEQ ID NO:140 is the determined cDNA sequence of 13142  
SEQ ID NO:141 is the determined cDNA sequence of 14376  
SEQ ID NO:142 is the determined cDNA sequence of 14377  
15 SEQ ID NO:143 is the determined cDNA sequence of 14383  
SEQ ID NO:144 is the determined cDNA sequence of 14384  
SEQ ID NO:145 is the determined cDNA sequence of 14387  
SEQ ID NO:146 is the determined cDNA sequence of 14392  
SEQ ID NO:147 is the determined cDNA sequence of 14394  
20 SEQ ID NO:148 is the determined cDNA sequence of 14398  
SEQ ID NO:149 is the determined cDNA sequence of 14401  
SEQ ID NO:150 is the determined cDNA sequence of 14402  
SEQ ID NO:151 is the determined cDNA sequence of 14405  
SEQ ID NO:152 is the determined cDNA sequence of 14409  
25 SEQ ID NO:153 is the determined cDNA sequence of 14412  
SEQ ID NO:154 is the determined cDNA sequence of 14414  
SEQ ID NO:155 is the determined cDNA sequence of 14415  
SEQ ID NO:156 is the determined cDNA sequence of 14416  
SEQ ID NO:157 is the determined cDNA sequence of 14419  
30 SEQ ID NO:158 is the determined cDNA sequence of 14426  
SEQ ID NO:159 is the determined cDNA sequence of 14427  
SEQ ID NO:160 is the determined cDNA sequence of 14375

- SEQ ID NO:161 is the determined cDNA sequence of 14378  
SEQ ID NO:162 is the determined cDNA sequence of 14379  
SEQ ID NO:163 is the determined cDNA sequence of 14380  
SEQ ID NO:164 is the determined cDNA sequence of 14381  
5 SEQ ID NO:165 is the determined cDNA sequence of 14382  
SEQ ID NO:166 is the determined cDNA sequence of 14388  
SEQ ID NO:167 is the determined cDNA sequence of 14399  
SEQ ID NO:168 is the determined cDNA sequence of 14406  
SEQ ID NO:169 is the determined cDNA sequence of 14407  
10 SEQ ID NO:170 is the determined cDNA sequence of 14408  
SEQ ID NO:171 is the determined cDNA sequence of 14417  
SEQ ID NO:172 is the determined cDNA sequence of 14418  
SEQ ID NO:173 is the determined cDNA sequence of 14423  
SEQ ID NO:174 is the determined cDNA sequence of 14424  
15 SEQ ID NO:175 is the determined cDNA sequence of B726P-20  
SEQ ID NO:176 is the predicted amino acid sequence of B726P-20 (also referred to as B726P downstream ORF)  
SEQ ID NO:177 is a PCR primer  
SEQ ID NO:178 is the determined cDNA sequence of B726P-74  
20 SEQ ID NO:179 is the predicted amino acid sequence of B726P-74  
SEQ ID NO:180 is the determined cDNA sequence of B726P-79  
SEQ ID NO:181 is the predicted amino acid sequence of B726P-79  
SEQ ID NO:182 is the determined cDNA sequence of 19439.1, showing  
homology to the mammaglobin gene  
25 SEQ ID NO:183 is the determined cDNA sequence of 19407.1, showing  
homology to the human keratin gene  
SEQ ID NO:184 is the determined cDNA sequence of 19428.1, showing  
homology to human chromosome 17 clone  
SEQ ID NO:185 is the determined cDNA sequence of B808P (19408),  
30 showing no significant homology to any known gene  
SEQ ID NO:186 is the determined cDNA sequence of 19460.1, showing  
no significant homology to any known gene

SEQ ID NO:187 is the determined cDNA sequence of 19419.1, showing  
homology to Ig kappa light chain

SEQ ID NO:188 is the determined cDNA sequence of 19411.1, showing  
homology to human alpha-1 collagen

5           SEQ ID NO:189 is the determined cDNA sequence of 19420.1, showing  
homology to mus musculus proteinase-3

SEQ ID NO:190 is the determined cDNA sequence of 19432.1, showing  
homology to human high motility group box

10           SEQ ID NO:191 is the determined cDNA sequence of 19412.1, showing  
homology to the human plasminogen activator gene

SEQ ID NO:192 is the determined cDNA sequence of 19415.1, showing  
homology to mitogen activated protein kinase

SEQ ID NO:193 is the determined cDNA sequence of 19409.1, showing  
homology to the chondroitin sulfate proteoglycan protein

15           SEQ ID NO:194 is the determined cDNA sequence of 19406.1, showing  
no significant homology to any known gene

SEQ ID NO:195 is the determined cDNA sequence of 19421.1, showing  
homology to human fibronectin

20           SEQ ID NO:196 is the determined cDNA sequence of 19426.1, showing  
homology to the retinoic acid receptor responder 3

SEQ ID NO:197 is the determined cDNA sequence of 19425.1, showing  
homology to MyD88 mRNA

SEQ ID NO:198 is the determined cDNA sequence of 19424.1, showing  
homology to peptide transporter (TAP-1) mRNA

25           SEQ ID NO:199 is the determined cDNA sequence of 19429.1, showing  
no significant homology to any known gene

SEQ ID NO:200 is the determined cDNA sequence of 19435.1, showing  
homology to human polymorphic epithelial mucin

30           SEQ ID NO:201 is the determined cDNA sequence of B813P (19434.1),  
showing homology to human GATA-3 transcription factor

SEQ ID NO:202 is the determined cDNA sequence of 19461.1, showing  
homology to the human AP-2 gene

SEQ ID NO:203 is the determined cDNA sequence of 19450.1, showing homology to DNA binding regulatory factor

SEQ ID NO:204 is the determined cDNA sequence of 19451.1, showing homology to Na/H exchange regulatory co-factor

5        SEQ ID NO:205 is the determined cDNA sequence of 19462.1, showing no significant homology to any known gene

SEQ ID NO:206 is the determined cDNA sequence of 19455.1, showing homology to human mRNA for histone HAS.Z

10       SEQ ID NO:207 is the determined cDNA sequence of 19459.1, showing homology to PAC clone 179N16

SEQ ID NO:208 is the determined cDNA sequence of 19464.1, showing no significant homology to any known gene

SEQ ID NO:209 is the determined cDNA sequence of 19414.1, showing homology to lipophilin B

15       SEQ ID NO:210 is the determined cDNA sequence of 19413.1, showing homology to chromosome 17 clone hRPK.209\_J\_20

SEQ ID NO:211 is the determined cDNA sequence of 19416.1, showing no significant homology to any known gene

20       SEQ ID NO:212 is the determined cDNA sequence of 19437.1, showing homology to human clone 24976 mRNA

SEQ ID NO:213 is the determined cDNA sequence of 19449.1, showing homology to mouse DNA for PG-M core protein

SEQ ID NO:214 is the determined cDNA sequence of 19446.1, showing no significant homology to any known gene

25       SEQ ID NO:215 is the determined cDNA sequence of 19452.1, showing no significant homology to any known gene

SEQ ID NO:216 is the determined cDNA sequence of 19483.1, showing no significant homology to any known gene

30       SEQ ID NO:217 is the determined cDNA sequence of 19526.1, showing homology to human lipophilin C

SEQ ID NO:218 is the determined cDNA sequence of 19484.1, showing homology to the secreted cement gland protein XAG-2

SEQ ID NO:219 is the determined cDNA sequence of 19470.1, showing no significant homology to any known gene

SEQ ID NO:220 is the determined cDNA sequence of 19469.1, showing homology to the human HLA-DM gene

5 SEQ ID NO:221 is the determined cDNA sequence of 19482.1, showing homology to the human pS2 protein gene

SEQ ID NO:222 is the determined cDNA sequence of B805P (19468.1), showing no significant homology to any known gene

10 SEQ ID NO:223 is the determined cDNA sequence of 19467.1, showing homology to human thrombospondin mRNA

SEQ ID NO:224 is the determined cDNA sequence of 19498.1, showing homology to the CDC2 gene involved in cell cycle control

SEQ ID NO:225 is the determined cDNA sequence of 19506.1, showing homology to human cDNA for TREB protein

15 SEQ ID NO:226 is the determined cDNA sequence of B806P (19505.1), showing no significant homology to any known gene

SEQ ID NO:227 is the determined cDNA sequence of 19486.1, showing homology to type I epidermal keratin

20 SEQ ID NO:228 is the determined cDNA sequence of 19510.1, showing homology to glucose transporter for glycoprotein

SEQ ID NO:229 is the determined cDNA sequence of 19512.1, showing homology to the human lysyl hydroxylase gene

SEQ ID NO:230 is the determined cDNA sequence of 19511.1, showing homology to human palmitoyl-protein thioesterase

25 SEQ ID NO:231 is the determined cDNA sequence of 19508.1, showing homology to human alpha enolase

SEQ ID NO:232 is the determined cDNA sequence of B807P (19509.1), showing no significant homology to any known gene

30 SEQ ID NO:233 is the determined cDNA sequence of B809P (19520.1), showing homology to clone 102D24 on chromosome 11q13.31

SEQ ID NO:234 is the determined cDNA sequence of 19507.1, showing homology to prosome beta-subunit

SEQ ID NO:235 is the determined cDNA sequence of 19525.1, showing homology to human pro-urokinase precursor

SEQ ID NO:236 is the determined cDNA sequence of 19513.1, showing no significant homology to any known gene

5           SEQ ID NO:237 is the determined cDNA sequence of 19517.1, showing homology to human PAC 128M19 clone

SEQ ID NO:238 is the determined cDNA sequence of 19564.1, showing homology to human cytochrome P450-IIB

10           SEQ ID NO:239 is the determined cDNA sequence of 19553.1, showing homology to human GABA-A receptor pi subunit

SEQ ID NO:240 is the determined cDNA sequence of B811P (19575.1), showing no significant homology to any known gene

SEQ ID NO:241 is the determined cDNA sequence of B810P (19560.1), showing no significant homology to any known gene

15           SEQ ID NO:242 is the determined cDNA sequence of 19588.1, showing homology to aortic carboxypeptidase-like protein

SEQ ID NO:243 is the determined cDNA sequence of 19551.1, showing homology to human BCL-1 gene

20           SEQ ID NO:244 is the determined cDNA sequence of 19567.1, showing homology to human proteasome-related mRNA

SEQ ID NO:245 is the determined cDNA sequence of B803P (19583.1), showing no significant homology to any known gene

SEQ ID NO:246 is the determined cDNA sequence of B812P (19587.1), showing no significant homology to any known gene

25           SEQ ID NO:247 is the determined cDNA sequence of B802P (19392.2), showing homology to human chromosome 17

SEQ ID NO:248 is the determined cDNA sequence of 19393.2, showing homology to human nicein B2 chain

30           SEQ ID NO:249 is the determined cDNA sequence of 19398.2, human MHC class II DQ alpha mRNA

SEQ ID NO:250 is the determined cDNA sequence of B804P (19399.2), showing homology to human Xp22 BAC GSHB-184P14

SEQ ID NO:251 is the determined cDNA sequence of 19401.2, showing homology to human ikB kinase-b gene

SEQ ID NO:252 is the determined cDNA sequence of 20266, showing no significant homology to any known gene

5           SEQ ID NO:253 is the determined cDNA sequence of B826P (20270), showing no significant homology to any known gene

SEQ ID NO:254 is the determined cDNA sequence of 20274, showing no significant homology to any known gene

10           SEQ ID NO:255 is the determined cDNA sequence of 20276, showing no significant homology to any known gene

SEQ ID NO:256 is the determined cDNA sequence of 20277, showing no significant homology to any known gene

SEQ ID NO:257 is the determined cDNA sequence of B823P (20280), showing no significant homology to any known gene

15           SEQ ID NO:258 is the determined cDNA sequence of B821P (20281), showing no significant homology to any known gene

SEQ ID NO:259 is the determined cDNA sequence of B824P (20294), showing no significant homology to any known gene

20           SEQ ID NO:260 is the determined cDNA sequence of 20303, showing no significant homology to any known gene

SEQ ID NO:261 is the determined cDNA sequence of B820P (20310), showing no significant homology to any known gene

SEQ ID NO:262 is the determined cDNA sequence of B825P (20336), showing no significant homology to any known gene

25           SEQ ID NO:263 is the determined cDNA sequence of B827P (20341), showing no significant homology to any known gene

SEQ ID NO:264 is the determined cDNA sequence of 20941, showing no significant homology to any known gene

30           SEQ ID NO:265 is the determined cDNA sequence of 20954, showing no significant homology to any known gene

SEQ ID NO:266 is the determined cDNA sequence of 20961, showing no significant homology to any known gene

SEQ ID NO:267 is the determined cDNA sequence of 20965, showing no significant homology to any known gene

SEQ ID NO:268 is the determined cDNA sequence of 20975, showing no significant homology to any known gene

5 SEQ ID NO:269 is the determined cDNA sequence of 20261, showing homology to Human p120 catenin

SEQ ID NO:270 is the determined cDNA sequence of B822P (20262), showing homology to Human membrane glycoprotein 4F2

10 SEQ ID NO:271 is the determined cDNA sequence of 20265, showing homology to Human Na, K-ATPase Alpha 1

SEQ ID NO:272 is the determined cDNA sequence of 20267, showing homology to Human heart HS 90, partial cds

SEQ ID NO:273 is the determined cDNA sequence of 20268, showing homology to Human mRNA GPI-anchored protein p137

15 SEQ ID NO:274 is the determined cDNA sequence of 20271, showing homology to Human cleavage stimulation factor 77 kDa subunit

SEQ ID NO:275 is the determined cDNA sequence of 20272, showing homology to Human p190-B

20 SEQ ID NO:276 is the determined cDNA sequence of 20273, showing homology to Human ribophorin

SEQ ID NO:277 is the determined cDNA sequence of 20278, showing homology to Human ornithine amino transferase

SEQ ID NO:278 is the determined cDNA sequence of 20279, showing homology to Human S-adenosylmethionine synthetase

25 SEQ ID NO:279 is the determined cDNA sequence of 20293, showing homology to Human x inactivation transcript

SEQ ID NO:280 is the determined cDNA sequence of 20300, showing homology to Human cytochrome p450

30 SEQ ID NO:281 is the determined cDNA sequence of 20305, showing homology to Human elongation factor-1 alpha

SEQ ID NO:282 is the determined cDNA sequence of 20306, showing homology to Human epithelial ets protein

SEQ ID NO:283 is the determined cDNA sequence of 20307, showing homology to Human signal transducer mRNA

SEQ ID NO:284 is the determined cDNA sequence of 20313, showing homology to Human GABA-A receptor pi subunit mRNA

5 SEQ ID NO:285 is the determined cDNA sequence of 20317, showing homology to Human tyrosine phosphatase

SEQ ID NO:286 is the determined cDNA sequence of 20318, showing homology to Human cathepsine B proteinase

10 SEQ ID NO:287 is the determined cDNA sequence of 20320, showing homology to Human 2-phosphopyruvate-hydratase-alpha-enolase

SEQ ID NO:288 is the determined cDNA sequence of 20321, showing homology to Human E-cadherin

SEQ ID NO:289 is the determined cDNA sequence of 20322, showing homology to Human hsp86

15 SEQ ID NO:290 is the determined cDNA sequence of B828P (20326), showing homology to Human x inactivation transcript

SEQ ID NO:291 is the determined cDNA sequence of 20333, showing homology to Human chromatin regulator, SMARCA5

20 SEQ ID NO:292 is the determined cDNA sequence of 20335, showing homology to Human sphingolipid activator protein 1

SEQ ID NO:293 is the determined cDNA sequence of 20337, showing homology to Human hepatocyte growth factor activator inhibitor type 2

SEQ ID NO:294 is the determined cDNA sequence of 20338, showing homology to Human cell adhesion molecule CD44

25 SEQ ID NO:295 is the determined cDNA sequence of 20340, showing homology to Human nuclear factor (erythroid-derived)-like 1

SEQ ID NO:296 is the determined cDNA sequence of 20938, showing homology to Human vinculin mRNA

30 SEQ ID NO:297 is the determined cDNA sequence of 20939, showing homology to Human elongation factor EF-1-alpha

SEQ ID NO:298 is the determined cDNA sequence of 20940, showing homology to Human nestin gene

SEQ ID NO:299 is the determined cDNA sequence of 20942, showing homology to Human pancreatic ribonuclease

SEQ ID NO:300 is the determined cDNA sequence of 20943, showing homology to Human transcobalamin I

5           SEQ ID NO:301 is the determined cDNA sequence of 20944, showing homology to Human beta-tubulin

SEQ ID NO:302 is the determined cDNA sequence of 20946, showing homology to Human HS1 protein

10           SEQ ID NO:303 is the determined cDNA sequence of 20947, showing homology to Human cathepsin B

SEQ ID NO:304 is the determined cDNA sequence of 20948, showing homology to Human testis enhanced gene transcript

SEQ ID NO:305 is the determined cDNA sequence of 20949, showing homology to Human elongation factor EF-1-alpha

15           SEQ ID NO:306 is the determined cDNA sequence of 20950, showing homology to Human ADP-ribosylation factor 3

SEQ ID NO:307 is the determined cDNA sequence of 20951, showing homology to Human IFP53 or WRS for tryptophanyl-tRNA synthetase

20           SEQ ID NO:308 is the determined cDNA sequence of 20952, showing homology to Human cyclin-dependent protein kinase

SEQ ID NO:309 is the determined cDNA sequence of 20957, showing homology to Human alpha-tubulin isoform 1

SEQ ID NO:310 is the determined cDNA sequence of 20959, showing homology to Human tyrosine phosphatase-61bp deletion

25           SEQ ID NO:311 is the determined cDNA sequence of 20966, showing homology to Human tyrosine phosphatase

SEQ ID NO:312 is the determined cDNA sequence of B830P (20976), showing homology to Human nuclear factor NF 45

30           SEQ ID NO:313 is the determined cDNA sequence of B829P (20977), showing homology to Human delta-6 fatty acid desaturase

SEQ ID NO:314 is the determined cDNA sequence of 20978, showing homology to Human nuclear aconitase

SEQ ID NO:315 is the determined cDNA sequence of clone 23176.  
SEQ ID NO:316 is the determined cDNA sequence of clone 23140.  
SEQ ID NO:317 is the determined cDNA sequence of clone 23166.  
SEQ ID NO:318 is the determined cDNA sequence of clone 23167.  
5 SEQ ID NO:319 is the determined cDNA sequence of clone 23177.  
SEQ ID NO:320 is the determined cDNA sequence of clone 23217.  
SEQ ID NO:321 is the determined cDNA sequence of clone 23169.  
SEQ ID NO:322 is the determined cDNA sequence of clone 23160.  
SEQ ID NO:323 is the determined cDNA sequence of clone 23182.  
10 SEQ ID NO:324 is the determined cDNA sequence of clone 23232.  
SEQ ID NO:325 is the determined cDNA sequence of clone 23203.  
SEQ ID NO:326 is the determined cDNA sequence of clone 23198.  
SEQ ID NO:327 is the determined cDNA sequence of clone 23224.  
SEQ ID NO:328 is the determined cDNA sequence of clone 23142.  
15 SEQ ID NO:329 is the determined cDNA sequence of clone 23138.  
SEQ ID NO:330 is the determined cDNA sequence of clone 23147.  
SEQ ID NO:331 is the determined cDNA sequence of clone 23148.  
SEQ ID NO:332 is the determined cDNA sequence of clone 23149.  
SEQ ID NO:333 is the determined cDNA sequence of clone 23172.  
20 SEQ ID NO:334 is the determined cDNA sequence of clone 23158.  
SEQ ID NO:335 is the determined cDNA sequence of clone 23156.  
SEQ ID NO:336 is the determined cDNA sequence of clone 23221.  
SEQ ID NO:337 is the determined cDNA sequence of clone 23223.  
SEQ ID NO:338 is the determined cDNA sequence of clone 23155.  
25 SEQ ID NO:339 is the determined cDNA sequence of clone 23225.  
SEQ ID NO:340 is the determined cDNA sequence of clone 23226.  
SEQ ID NO:341 is the determined cDNA sequence of clone 23228.  
SEQ ID NO:342 is the determined cDNA sequence of clone 23229.  
SEQ ID NO:343 is the determined cDNA sequence of clone 23231.  
30 SEQ ID NO:344 is the determined cDNA sequence of clone 23154.  
SEQ ID NO:345 is the determined cDNA sequence of clone 23157.  
SEQ ID NO:346 is the determined cDNA sequence of clone 23153.

SEQ ID NO:347 is the determined cDNA sequence of clone 23159.  
SEQ ID NO:348 is the determined cDNA sequence of clone 23152.  
SEQ ID NO:349 is the determined cDNA sequence of clone 23161.  
SEQ ID NO:350 is the determined cDNA sequence of clone 23162.  
5 SEQ ID NO:351 is the determined cDNA sequence of clone 23163.  
SEQ ID NO:352 is the determined cDNA sequence of clone 23164.  
SEQ ID NO:353 is the determined cDNA sequence of clone 23165.  
SEQ ID NO:354 is the determined cDNA sequence of clone 23151.  
SEQ ID NO:355 is the determined cDNA sequence of clone 23150.  
10 SEQ ID NO:356 is the determined cDNA sequence of clone 23168.  
SEQ ID NO:357 is the determined cDNA sequence of clone 23146.  
SEQ ID NO:358 is the determined cDNA sequence of clone 23170.  
SEQ ID NO:359 is the determined cDNA sequence of clone 23171.  
SEQ ID NO:360 is the determined cDNA sequence of clone 23145.  
15 SEQ ID NO:361 is the determined cDNA sequence of clone 23174.  
SEQ ID NO:362 is the determined cDNA sequence of clone 23175.  
SEQ ID NO:363 is the determined cDNA sequence of clone 23144.  
SEQ ID NO:364 is the determined cDNA sequence of clone 23178.  
SEQ ID NO:365 is the determined cDNA sequence of clone 23179.  
20 SEQ ID NO:366 is the determined cDNA sequence of clone 23180.  
SEQ ID NO:367 is the determined cDNA sequence of clone 23181.  
SEQ ID NO:368 is the determined cDNA sequence of clone 23143.  
SEQ ID NO:369 is the determined cDNA sequence of clone 23183.  
SEQ ID NO:370 is the determined cDNA sequence of clone 23184.  
25 SEQ ID NO:371 is the determined cDNA sequence of clone 23185.  
SEQ ID NO:372 is the determined cDNA sequence of clone 23186.  
SEQ ID NO:373 is the determined cDNA sequence of clone 23187.  
SEQ ID NO:374 is the determined cDNA sequence of clone 23190.  
SEQ ID NO:375 is the determined cDNA sequence of clone 23189.  
30 SEQ ID NO:376 is the determined cDNA sequence of clone 23202.  
SEQ ID NO:378 is the determined cDNA sequence of clone 23191.  
SEQ ID NO:379 is the determined cDNA sequence of clone 23188.

SEQ ID NO:380 is the determined cDNA sequence of clone 23194.  
SEQ ID NO:381 is the determined cDNA sequence of clone 23196.  
SEQ ID NO:382 is the determined cDNA sequence of clone 23195.  
SEQ ID NO:383 is the determined cDNA sequence of clone 23193.  
5 SEQ ID NO:384 is the determined cDNA sequence of clone 23199.  
SEQ ID NO:385 is the determined cDNA sequence of clone 23200.  
SEQ ID NO:386 is the determined cDNA sequence of clone 23192.  
SEQ ID NO:387 is the determined cDNA sequence of clone 23201.  
SEQ ID NO:388 is the determined cDNA sequence of clone 23141.  
10 SEQ ID NO:389 is the determined cDNA sequence of clone 23139.  
SEQ ID NO:390 is the determined cDNA sequence of clone 23204.  
SEQ ID NO:391 is the determined cDNA sequence of clone 23205.  
SEQ ID NO:392 is the determined cDNA sequence of clone 23206.  
SEQ ID NO:393 is the determined cDNA sequence of clone 23207.  
15 SEQ ID NO:394 is the determined cDNA sequence of clone 23208.  
SEQ ID NO:395 is the determined cDNA sequence of clone 23209.  
SEQ ID NO:396 is the determined cDNA sequence of clone 23210.  
SEQ ID NO:397 is the determined cDNA sequence of clone 23211.  
SEQ ID NO:398 is the determined cDNA sequence of clone 23212.  
20 SEQ ID NO:399 is the determined cDNA sequence of clone 23214.  
SEQ ID NO:400 is the determined cDNA sequence of clone 23215.  
SEQ ID NO:401 is the determined cDNA sequence of clone 23216.  
SEQ ID NO:402 is the determined cDNA sequence of clone 23137.  
SEQ ID NO:403 is the determined cDNA sequence of clone 23218.  
25 SEQ ID NO:404 is the determined cDNA sequence of clone 23220.  
SEQ ID NO:405 is the determined cDNA sequence of clone 19462.  
SEQ ID NO:406 is the determined cDNA sequence of clone 19430.  
SEQ ID NO:407 is the determined cDNA sequence of clone 19407.  
SEQ ID NO:408 is the determined cDNA sequence of clone 19448.  
30 SEQ ID NO:409 is the determined cDNA sequence of clone 19447.  
SEQ ID NO:410 is the determined cDNA sequence of clone 19426.  
SEQ ID NO:411 is the determined cDNA sequence of clone 19441.

SEQ ID NO:412 is the determined cDNA sequence of clone 19454.  
SEQ ID NO:413 is the determined cDNA sequence of clone 19463.  
SEQ ID NO:414 is the determined cDNA sequence of clone 19419.  
SEQ ID NO:415 is the determined cDNA sequence of clone 19434.  
5 SEQ ID NO:416 is the determined extended cDNA sequence of B820P.  
SEQ ID NO:417 is the determined extended cDNA sequence of B821P.  
SEQ ID NO:418 is the determined extended cDNA sequence of B822P.  
SEQ ID NO:419 is the determined extended cDNA sequence of B823P.  
SEQ ID NO:420 is the determined extended cDNA sequence of B824P.  
10 SEQ ID NO:421 is the determined extended cDNA sequence of B825P.  
SEQ ID NO:422 is the determined extended cDNA sequence of B826P.  
SEQ ID NO:423 is the determined extended cDNA sequence of B827P.  
SEQ ID NO:424 is the determined extended cDNA sequence of B828P.  
SEQ ID NO:425 is the determined extended cDNA sequence of B829P.  
15 SEQ ID NO:426 is the determined extended cDNA sequence of B830P.  
SEQ ID NO:427 is the determined cDNA sequence of clone 266B4.  
SEQ ID NO:428 is the determined cDNA sequence of clone 22892.  
SEQ ID NO:429 is the determined cDNA sequence of clone 266G3.  
SEQ ID NO:430 is the determined cDNA sequence of clone 22890.  
20 SEQ ID NO:431 is the determined cDNA sequence of clone 264B4.  
SEQ ID NO:432 is the determined cDNA sequence of clone 22883.  
SEQ ID NO:433 is the determined cDNA sequence of clone 22882.  
SEQ ID NO:434 is the determined cDNA sequence of clone 22880.  
SEQ ID NO:435 is the determined cDNA sequence of clone 263G1.  
25 SEQ ID NO:436 is the determined cDNA sequence of clone 263G6.  
SEQ ID NO:437 is the determined cDNA sequence of clone 262B2.  
SEQ ID NO:438 is the determined cDNA sequence of clone 262B6.  
SEQ ID NO:439 is the determined cDNA sequence of clone 22869.  
SEQ ID NO:440 is the determined cDNA sequence of clone 21374.  
30 SEQ ID NO:441 is the determined cDNA sequence of clone 21362.  
SEQ ID NO:442 is the determined cDNA sequence of clone 21349.  
SEQ ID NO:443 is the determined cDNA sequence of clone 21309.

SEQ ID NO:444 is the determined cDNA sequence of clone 21097.  
SEQ ID NO:445 is the determined cDNA sequence of clone 21096.  
SEQ ID NO:446 is the determined cDNA sequence of clone 21094.  
SEQ ID NO:447 is the determined cDNA sequence of clone 21093.  
5 SEQ ID NO:448 is the determined cDNA sequence of clone 21091.  
SEQ ID NO:449 is the determined cDNA sequence of clone 21089.  
SEQ ID NO:450 is the determined cDNA sequence of clone 21087.  
SEQ ID NO:451 is the determined cDNA sequence of clone 21085.  
SEQ ID NO:452 is the determined cDNA sequence of clone 21084.  
10 SEQ ID NO:453 is a first partial cDNA sequence of clone 2BT1-40.  
SEQ ID NO:454 is a second partial cDNA sequence of clone 2BT1-40.  
SEQ ID NO:455 is the determined cDNA sequence of clone 21063.  
SEQ ID NO:456 is the determined cDNA sequence of clone 21062.  
SEQ ID NO:457 is the determined cDNA sequence of clone 21060.  
15 SEQ ID NO:458 is the determined cDNA sequence of clone 21053.  
SEQ ID NO:459 is the determined cDNA sequence of clone 21050.  
SEQ ID NO:460 is the determined cDNA sequence of clone 21036.  
SEQ ID NO:461 is the determined cDNA sequence of clone 21037.  
SEQ ID NO:462 is the determined cDNA sequence of clone 21048.  
20 SEQ ID NO:463 is a consensus DNA sequence of B726P (referred to as  
B726P-spliced\_seq\_B726P).  
SEQ ID NO:464 is the determined cDNA sequence of a second splice  
form of B726P (referred to as 27490.seq\_B726P).  
SEQ ID NO:465 is the determined cDNA sequence of a third splice form  
25 of B726P (referred to as 27068.seq\_B726P).  
SEQ ID NO:466 is the determined cDNA sequence of a second splice  
form of B726P (referred to as 23113.seq\_B726P).  
SEQ ID NO:467 is the determined cDNA sequence of a second splice  
form of B726P (referred to as 23103.seq\_B726P).  
30 SEQ ID NO:468 is the determined cDNA sequence of a second splice  
form of B726P (referred to as 19310.seq\_B726P).

SEQ ID NO:469 is the predicted amino acid sequence encoded by the upstream ORF of SEQ ID NO:463.

SEQ ID NO:470 is the predicted amino acid sequence encoded by SEQ ID NO:464.

5 SEQ ID NO:471 is the predicted amino acid sequence encoded by SEQ ID NO:465.

SEQ ID NO:472 is the predicted amino acid sequence encoded by SEQ ID NO:466.

10 SEQ ID NO:473 is the predicted amino acid sequence encoded by SEQ ID NO:467.

SEQ ID NO:474 is the determined cDNA sequence for an alternative splice form of B726P.

SEQ ID NO:475 is the amino acid sequence encoded by SEQ ID NO:474.

15 SEQ ID NO:476 is the isolated cDNA sequence of B720P.

SEQ ID NO:477 is the cDNA sequence of a known keratin gene.

SEQ ID NO:478 is the amino acid sequence encoded by SEQ ID NO:477.

SEQ ID NO:479 is the determined cDNA sequence for clone 19465.

20 SEQ ID NO:480 and 481 are PCR primers.

SEQ ID NO:482 is the cDNA sequence for the expressed downstream ORF of B726P.

SEQ ID NO:483 is the amino acid sequence for the expressed recombinant downstream ORF of B726P.

25 SEQ ID NO:484 is the determined full-length cDNA sequence for B720P.

SEQ ID NO:485 is the amino acid sequence encoded by SEQ ID NO:484.

30 SEQ ID NO:486 is the determined cDNA sequence of a truncated form of B720P, referred to as B720P-tr.

SEQ ID NO:487 is the amino acid sequence of B720P-tr.

SEQ ID NO:488 is the amino acid sequence of a naturally processed epitope of B726P recognized by B726P-specific CTL.

SEQ ID NO:489 is a DNA sequence encoding the B726P epitope set forth in SEQ ID NO:488.

5           SEQ ID NO:490 is a DNA sequence encoding a fusion protein wherein mammaglobin is fused to the B726P combined upstream and downstream open reading frame (ORF) (the amino acid sequence of the B726P combined ORF is disclosed herein as SEQ ID NO:475 which is encoded by the DNA sequence of SEQ ID NO:474).

10           SEQ ID NO:491 is a DNA sequence encoding a fusion protein wherein mammaglobin is fused to the B726P upstream ORF (the amino acid sequence of the B726P upstream ORF is disclosed herein as SEQ ID NO:469 which is encoded by the DNA sequence of SEQ ID NO:463).

15           SEQ ID NO:492 is a DNA sequence encoding a fusion protein wherein mammaglobin is fused to the B726P downstream ORF (the amino acid sequence of the B726P downstream ORF is disclosed herein as SEQ ID NO:176 which is encoded by the DNA sequence of SEQ ID NO:175).

            SEQ ID NO:493 is the amino acid sequence encoded by the DNA sequence of SEQ ID NO:490.

20           SEQ ID NO:494 is the amino acid sequence encoded by the DNA sequence of SEQ ID NO:491.

            SEQ ID NO:495 is the amino acid sequence encoded by the DNA sequence of SEQ ID NO:492.

            SEQ ID NO:496 is amino acids 59-78 of SEQ ID NO:493.

            SEQ ID NO:497 is amino acids 55-69 of SEQ ID NO:493.

25           SEQ ID NO:498 is amino acids 13-33 of SEQ ID NO:493.

            SEQ ID NO:499 is amino acids 41-60 of SEQ ID NO:493.

            SEQ ID NO:500 is amino acids 2-10 of SEQ ID NO:493.

            SEQ ID NO:501 is amino acids 47-59 of SEQ ID NO:493.

            SEQ ID NO:502 is amino acids 62-74 of SEQ ID NO:493.

30           SEQ ID NO:503 is amino acids 1-93 of SEQ ID NO:493.

            SEQ ID NO:504 is the full-length cDNA sequence for B718P.

SEQ ID NO:505 is the cDNA sequence of the open reading frame of B718P including stop codon.

SEQ ID NO:506 is the cDNA sequence of the open reading frame of B718P without stop codon.

5           SEQ ID NO:507 is the full-length amino acid sequence of B718P.

SEQ ID NO:508 represents amino acids 1-158 of SEQ ID NO:507.

SEQ ID NO:509 represents amino acids 159-243 of SEQ ID NO:509.

SEQ ID NO:510 is the entire cDNA sequence of the open reading frame, including stop codon, of a first variant of B723P, referred to as B723P-short.

10           SEQ ID NO:511 is the entire cDNA sequence of the open reading frame, without stop codon, of a first variant of B723P, referred to as B723P-short.

SEQ ID NO:512 is the entire cDNA sequence of the open reading frame, including stop codon, of a second variant of B723P, referred to as B723P-long.

15           SEQ ID NO:513 is the entire cDNA sequence of the open reading frame, without stop codon, of a second variant of B723P, referred to as B723P-long.

SEQ ID NO:514 is the amino acid sequence of B723P-short.

SEQ ID NO:515 is the amino acid sequence of B723P-long.

SEQ ID NO:516 is amino acids 1-197 of B723P-short.

SEQ ID NO:517 is amino acids 1-232 of B723P-long.

20           SEQ ID NO:518 is amino acids 198-243 of B723P-short.

SEQ ID NO:519 is amino acids 218-243 of B723P-short.

SEQ ID NO:520 – 533 are the DNA sequences of epitopes of B726P.

SEQ ID NO:534-547 are the amino acid sequences of epitopes of B726P.

25           SEQ ID NO:548 is the cDNA sequence of B726P Combined ORF coding\_ region for expression in *E. coli*.

SEQ ID NO:549 is the cDNA sequence of B726P Upstream ORF coding\_ region for expression in *E. coli*.

SEQ ID NO:550 is the cDNA sequence of B726P Downstream ORF coding\_ region for expression in *E. coli*.

30           SEQ ID NO:551 is the amino acid sequence of B726P Downstream ORF encoded by the cDNA set forth in SEQ ID NO:550.

SEQ ID NO:552 is the amino acid sequence of B726P Upstream ORF with HIS, encoded by the cDNA set forth in SEQ ID NO:549.

SEQ ID NO:553 is the amino acid sequence of B726P Combined ORF correct, encoded by the cDNA set forth in SEQ ID NO:548.

5 SEQ ID NO:554-563 are PCR primers as described in Example 8.

SEQ ID NO:564 is the cDNA sequence for NY-BR-1, an extended sequence of B726P.

SEQ ID NO:565 is the amino acid sequence for NY-BR-1, an extended sequence of B726P, and encoded by the nucleotide sequence set forth in SEQ ID  
10 NO:564.

SEQ ID NO:566 is the cDNA sequence for B726P XC coding region with changes.

SEQ ID NO:567 is the cDNA sequence for B726P XB clone 83686 with 2 changes from the published NY-BR-1 sequence in SEQ ID NO:564.

15 SEQ ID NO:568 is the cDNA sequence for B726P XB clone 84330 with 4 changes from the published NY-BR-1 sequence in SEQ ID NO:564.

SEQ ID NO:569 is the cDNA sequence for B726P XB clone 84328 with 3 changes from the published NY-BR-1 sequence in SEQ ID NO:564.

SEQ ID NO:570 is the amino acid sequence for B726P XB clone 84328,  
20 encoded by the sequence set forth in SEQ ID NO:569.

SEQ ID NO:571 is the amino acid sequence for B726P XB clone 84330, encoded by the sequence set forth in SEQ ID NO:568.

SEQ ID NO:572 is the amino acid sequence for B726P XB clone 83686, encoded by the sequence set forth in SEQ ID NO:567.

25 SEQ ID NO:573 is the amino acid sequence for B726P XC, encoded by the sequence set forth in SEQ ID NO:566.

SEQ ID NO:574-575 are PCR primers as described in Example 12.

SEQ ID NO:576 is the full-length cDNA sequence for NY-BR-1.1.

SEQ ID NO:577 is the full-length amino acid sequence for NY-BR-1.1,  
30 encoded by the nucleotide sequence set forth in SEQ ID NO:576.

SEQ ID NO:578 is amino acids 289-308 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A2.1 antibody.

SEQ ID NO:579 is amino acids 225-244 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A19.1 antibody.

5           SEQ ID NO:580 is amino acids 232-252 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A19.1 and the 220A43 antibodies.

SEQ ID NO:581 is amino acids 73-92 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A94.1 antibody.

10           SEQ ID NO:582 is amino acids 145-164 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A151.1 and 220A86 antibodies.

SEQ ID NO:583 is amino acids 153-172 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A151.1 and 220A86 antibodies.

SEQ ID NO:584 is amino acids 1-20 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

15           SEQ ID NO:585 is amino acids 9-28 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

SEQ ID NO:586 is amino acids 17-36 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

20           SEQ ID NO:587 is amino acids 24-44 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

SEQ ID NO:588 is amino acids 97-116 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

SEQ ID NO:589 is amino acids 105-124 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

25           SEQ ID NO:590 is amino acids 113-132 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

SEQ ID NO:591 is amino acids 121-140 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

30           SEQ ID NO:592 is amino acids 129-148 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

SEQ ID NO:593 is amino acids 137-156 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

SEQ ID NO:594 is the amino acid sequence of peptide #2732 and corresponds to amino acids 1-20 of the B726P downstream ORF.

5        SEQ ID NO:595 is the amino acid sequence of peptide #2733 and corresponds to amino acids 11-30 of the B726P downstream ORF.

SEQ ID NO:596 is the amino acid sequence of peptide #2734 and corresponds to amino acids 21-40 of the B726P downstream ORF.

10       SEQ ID NO:597 is the amino acid sequence of peptide #2735 and corresponds to amino acids 31-50 of the B726P downstream ORF.

SEQ ID NO:598 is the amino acid sequence of peptide #2736 and corresponds to amino acids 41-60 of the B726P downstream ORF.

SEQ ID NO:599 is the amino acid sequence of peptide #2737 and corresponds to amino acids 51-70 of the B726P downstream ORF.

15       SEQ ID NO:600 is the amino acid sequence of peptide #2738 and corresponds to amino acids 61-80 of the B726P downstream ORF.

SEQ ID NO:601 is the amino acid sequence of peptide #2739 and corresponds to amino acids 71-90 of the B726P downstream ORF.

20       SEQ ID NO:602 is the amino acid sequence of peptide #2740 and corresponds to amino acids 81-100 of the B726P downstream ORF.

SEQ ID NO:603 is the amino acid sequence of peptide #2741 and corresponds to amino acids 91-110 of the B726P downstream ORF.

SEQ ID NO:604 is the amino acid sequence of peptide #2742 and corresponds to amino acids 101-120 of the B726P downstream ORF.

25       SEQ ID NO:605 is the amino acid sequence of peptide #2743 and corresponds to amino acids 111-130 of the B726P downstream ORF.

SEQ ID NO:606 is the amino acid sequence of peptide #2744 and corresponds to amino acids 121-140 of the B726P downstream ORF.

30       SEQ ID NO:607 is the amino acid sequence of peptide #2745 and corresponds to amino acids 130-151 of the B726P downstream ORF.

SEQ ID NO:608 is the amino acid sequence of peptide #2746 and corresponds to amino acids 141-160 of the B726P downstream ORF.

SEQ ID NO:609 is the amino acid sequence of peptide #2747 and corresponds to amino acids 151-170 of the B726P downstream ORF.

5        SEQ ID NO:610 is the amino acid sequence of peptide #2748 and corresponds to amino acids 161-180 of the B726P downstream ORF.

SEQ ID NO:611 is the amino acid sequence of peptide #2749 and corresponds to amino acids 170-190 of the B726P downstream ORF.

10       SEQ ID NO:612 is the amino acid sequence of peptide #2750 and corresponds to amino acids 181-200 of the B726P downstream ORF.

SEQ ID NO:613 is the amino acid sequence of peptide #2751 and corresponds to amino acids 191-210 of the B726P downstream ORF.

SEQ ID NO:614 is the amino acid sequence of peptide #2752 and corresponds to amino acids 201-220 of the B726P downstream ORF.

15       SEQ ID NO:615 is the amino acid sequence of peptide #2753 and corresponds to amino acids 211-230 of the B726P downstream ORF.

SEQ ID NO:616 is the amino acid sequence of peptide #2765 and corresponds to amino acids 221-240 of the B726P downstream ORF.

20       SEQ ID NO:617 is the amino acid sequence of peptide #2766 and corresponds to amino acids 231-250 of the B726P downstream ORF.

SEQ ID NO:618 is the amino acid sequence of peptide #2767 and corresponds to amino acids 240-260 of the B726P downstream ORF.

SEQ ID NO:619 is the amino acid sequence of peptide #2768 and corresponds to amino acids 251-270 of the B726P downstream ORF.

25       SEQ ID NO:620 is the amino acid sequence of peptide #2769 and corresponds to amino acids 261-280 of the B726P downstream ORF.

SEQ ID NO:621 is the amino acid sequence of peptide #2770 and corresponds to amino acids 271-290 of the B726P downstream ORF.

30       SEQ ID NO:622 is the amino acid sequence of peptide #2771 and corresponds to amino acids 281-300 of the B726P downstream ORF.

SEQ ID NO:623 is the amino acid sequence of peptide #2772 and corresponds to amino acids 291-310 of the B726P downstream ORF.

SEQ ID NO:624 is the amino acid sequence of peptide #2773 and corresponds to amino acids 298-317 of the B726P downstream ORF.

5 SEQ ID NO:625 is the amino acid sequence of peptide #3535 of B726P.

SEQ ID NO:626 is the amino acid sequence of peptide #3536 of B726P.

SEQ ID NO:627 is the amino acid sequence of peptide #3534 of B726P.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use  
10 in the therapy and diagnosis of cancer, particularly breast cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (*e.g.*, T cells).

15 The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning:  
20 A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal,  
25 A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether *supra* or *infra*, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates  
30 otherwise.

### Polypeptide Compositions

As used herein, the term "polypeptide" is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576. Certain other illustrative polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NO: 62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627.

The polypeptides of the present invention are sometimes herein referred to as breast tumor proteins or breast tumor polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in breast tumor samples. Thus, a "breast tumor polypeptide" or "breast tumor protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of breast tumor samples, for example preferably greater than about 20%, more preferably

greater than about 30%, and most preferably greater than about 50% or more of breast tumor samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal tissues, as determined using a representative assay provided herein. A breast tumor polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with breast cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide compositions set forth herein, such as those set forth in SEQ ID NO: 62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487,

488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576.

5           In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequences set forth  
10   herein.

          In one preferred embodiment, the polypeptide fragments and variants provide by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set for the herein.

          In another preferred embodiment, the polypeptide fragments and variants  
15   provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

          A polypeptide "variant," as the term is used herein, is a polypeptide that  
20   typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein and/or using any of a number of techniques well known in  
25   the art.

          For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino  
30   acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are:

isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5); glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

5           It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within  $\pm 2$  is preferred, those within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$   
10 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

15           As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0  $\pm$  1); glutamate (+3.0  $\pm$  1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5  $\pm$  1); alanine (−0.5); histidine (−0.5); cysteine (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−  
20 2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within  $\pm 2$  is preferred, those within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$  are even  
25 more particularly preferred.

          As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those  
30 of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of  
5 nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic  
10 nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may  
15 represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or  
20 alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally  
25 directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be  
30 "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two

sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a  
5 reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several  
10 alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology*  
15 vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and  
20 Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988)  
25 *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining  
30 percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402

and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for  
5 Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is  
10 reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in  
15 the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of  
20 matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises  
25 at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological  
30 and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to

desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements

responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

5           The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

10           In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is  
15 incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application  
20 60/158,585; *see also, Skeiky et al., Infection and Immun. (1999) 67:3998-4007*, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous immunogenic polypeptides with which it is fused. One preferred Ra12 fusion  
25 polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12  
30 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a

sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated

into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting  
5 signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4<sup>+</sup> T-cells specific for the polypeptide.

10 Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are  
15 synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and  
20 may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural  
25 system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

#### Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide  
30 compositions. The terms "DNA" and "polynucleotide" are used essentially

interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large  
5 chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and  
10 plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be  
15 DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules  
20 and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably and immunogenic variant or derivative, of such a sequence.

25 Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, complements of a polynucleotide sequence set forth in any one of SEQ ID  
30 NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, and degenerate variants of a

polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

5 In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%,  
10 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this invention using the methods described herein, (e.g., BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into  
15 account codon degeneracy, amino acid similarity, reading frame positioning and the like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished  
20 relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of  
25 sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate  
30 lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103,

*etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For

example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

5           When comparing polynucleotide sequences, two sequences are said to be “identical” if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A “comparison  
10 window” as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using  
15 the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical  
20 Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-  
25 425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988)  
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*Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

5                   One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent  
10                   sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of  
15                   the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for  
20                   nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

                  Preferably, the "percentage of sequence identity" is determined by  
25                   comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The  
30                   percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions,

dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be

obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and  
5 Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable  
10 signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known  
15 rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

20 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

25 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence  
30 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000

(including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in

length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

5           Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing  
10   selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

          The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or  
15   gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as  
20   provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

          Of course, for some applications, for example, where one desires to  
25   prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species  
30   can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered

more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

5           According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to  
10 the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear  
15 protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA<sub>A</sub> receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288).  
20 Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is  
25 capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the  
30 oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary,

and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure,  $T_m$ ,  
5 binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary  
10 to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997, 25(17):3389-402).

The use of an antisense delivery method employing a short peptide  
15 vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered  
20 into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme  
25 molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For  
30 example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an

oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide  
5 sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs  
10 through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to  
15 direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds  
20 to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity  
25 of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the  
30 specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis  $\delta$  virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of  
5 hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the hepatitis  $\delta$  virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada  
10 *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid  
15 molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

20 Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in  
25 other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO  
30 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can

be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the  
5 general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be  
10 directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical,  
15 systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s)  
20 within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the  
25 nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into  
30 mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA

vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem.* 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, *Bioorg Med Chem.* 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this  
5 difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

10 Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or  
15 for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*, Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug  
20 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*, Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S.  
25 Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.*  
30 (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the

relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, 5 mutational analysis, enhancers of transcription, nucleic acid purification, isolation of transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

#### Polynucleotide Identification, Characterization and Expression

Polynucleotides compositions of the present invention may be identified, 10 prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that 15 is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 20 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent 25 Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present 30 in a sample, the primers will bind to the target and the polymerase will cause the

primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR™ amplification technique, are readily known and available in the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed

libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5'

and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

5                   In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences  
10 may also be obtained by analysis of genomic fragments.

                  In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of  
15 the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

                  As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing  
20 non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

25                   Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene  
30 fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction

sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well

known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques  
5 are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York. N.Y.

A variety of expression vector/host systems may be utilized to contain  
10 and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus,  
15 CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out  
20 transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or  
25 PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

30 In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example,

when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence  
5 encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion  
10 proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at  
15 will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

20 In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of  
25 RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or  
30 Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are

appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*).

Additional selectable genes have been described, for example, *trpB*, which allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as  
5 anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that  
10 the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter.  
15 Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-  
20 RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies  
25 specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed.  
30 These and other assays are described, among other places, in Hampton, R. et al. (1990;

Serological Methods, a Laboratory Manual, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means  
5 for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA  
10 probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

15 Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the  
20 invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are  
25 not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego,  
30 Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion

protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase  
5 cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using  
10 solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length  
15 molecule.

#### Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant  
20 or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

25 Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant ( $K_d$ ) of the interaction, wherein a smaller  $K_d$  represents a greater  
30 affinity. Immunological binding properties of selected polypeptides can be quantified

using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" ( $K_{on}$ ) and the "off rate constant" ( $K_{off}$ ) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of  $K_{off}/K_{on}$  enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant  $K_d$ . See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

10           An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

25           Binding agents may be further capable of differentiating between patients with and without a cancer, such as breast cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g.,

blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each  
5 binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component,  
10 an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation  
15 of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.,* mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen  
20 without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically.  
25 Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J.*  
30 *Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the

desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab)<sub>2</sub>" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V<sub>H</sub>::V<sub>L</sub> heterodimer including an antigen-binding site which retains much

of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked  $V_H::V_L$  heterodimer which is expressed from a gene fusion including  $V_H$ - and  $V_L$ -encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural

features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) *Nature* 349:293-299; Lobuglio et al. (1989) *Proc. Nat. Acad. Sci. USA* 86:4220-4224; Shaw et al. (1987) *J Immunol.* 138:4534-4538; and Brown et al. (1987) *Cancer Res.* 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) *Nature* 332:323-327; Verhoeyen et al. (1988) *Science* 239:1534-1536; and Jones et al. (1986) *Nature* 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) *Ann. Rev. Biochem.* 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the

CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that  
5 comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in *Sequences of Proteins of Immunological Interest*, 4th ed., (U.S. Dept. of Health and Human Services, U.S.  
10 Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody  
15 molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the  
20 art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are  
25 thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary  
30 structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a

murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

### T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, 5 T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or 10 unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor 15 polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell 20 specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the 25 proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 30 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as

measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN- $\gamma$ ) is indicative of T cell activation (*see* Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

#### Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from

host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical  
5 compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and therapeutic  
10 vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

15 It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*,  
20 sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, *e.g.*, vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery  
25 systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable  
30 promoter and terminating signal). Alternatively, bacterial delivery systems may involve

the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L. (1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, *e.g.*, U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines* 90 (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129; Kotin, R. M. (1994) *Human Gene Therapy* 5:793-801; Shelling and Smith (1994) *Gene Therapy* 1:165-169; and Zhou et al. (1994) *J. Exp. Med.* 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK<sup>sup</sup>(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, *Proc. Natl. Acad. Sci. USA* (1990) 87:6743-6747; Fuerst et al. *Proc. Natl. Acad. Sci. USA* (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and

therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, e.g., WO 91/12882; WO 89/03429; and WO 92/03545.

5           Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

10           Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

          Additional illustrative information on these and other known viral-based  
15 delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science*  
20 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

          In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in the specific location and orientation  
25 via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host  
30 cell cycle. The manner in which the expression construct is delivered to a cell and

where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al.,  
5 *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described.  
10 In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder  
15 formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include  
20 those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the  
25 immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism,  
30 such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins.

Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL<sup>®</sup> adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin,

such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example  
5 combinations of at least two of the following group comprising QS21, QS7, Quil A,  $\beta$ -escin, or digitonin.

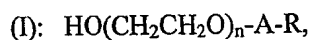
Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix,  
10 particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or  
15 suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol<sup>R</sup> to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the  
20 combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL<sup>®</sup> adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-MPL<sup>®</sup> adjuvant and tocopherol in an oil-in-water emulsion is described in WO  
25 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally  
30 comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhancyn<sup>®</sup>) (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

10 Other preferred adjuvants include adjuvant molecules of the general formula



wherein,  $n$  is 1-50,  $A$  is a bond or  $-\text{C}(\text{O})-$ ,  $R$  is  $\text{C}_{1-50}$  alkyl or Phenyl  $\text{C}_{1-50}$  alkyl.

One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein  $n$  is between 1 and 50, preferably 4-24, most preferably 9; the  $R$  component is  $\text{C}_{1-50}$ , preferably  $\text{C}_4\text{-C}_{20}$  alkyl and most preferably  $\text{C}_{12}$  alkyl, and  $A$  is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck index (12<sup>th</sup> edition: entry 7717). These adjuvant molecules are described in WO 25 99/52549.

The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

30 According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs),

such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be  
5 immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic  
10 cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*,  
15 with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As  
20 an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph  
25 nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into  
30 dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ ,

CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier

will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

5 Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the  
10 level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer  
15 comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

20 In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems.  
25 such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

30 The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered

saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent,

such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to  
5 materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds  
10 may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of  
15 active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a  
20 variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as  
25 one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

30 In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even

intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably  
5 mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include  
10 sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms,  
15 such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or  
20 by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in  
25 the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are  
30 especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will

be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-  
5 1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed  
10 herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be  
15 derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

20 The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active  
25 ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be  
30 delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the

lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in  
5 the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of  
10 the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as  
15 potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998 Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent  
20 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition,  
25 liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear to be associated with autoimmune responses or unacceptable  
30 toxicity after systemic delivery.

In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

Alternatively, in other embodiments, the invention provides for  
5 pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1  $\mu\text{m}$ ) may be designed using  
10 polymers able to be degraded *in vivo*. Such particles can be made as described, for example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

#### Cancer Therapeutic Methods

15 In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of breast cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer.  
20 Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the  
25 pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous  
30 host immune system to react against tumors with the administration of immune

response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established  
5 tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-  
10 activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic  
15 antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with  
20 retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for  
25 immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a  
30 recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies

have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical

outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard  
5 proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more breast tumor proteins and/or polynucleotides encoding such proteins in a  
10 biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as breast cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the  
15 biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a breast tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in  
20 the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c)  
25 comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding  
30 agent/polypeptide complex. Such detection reagents may comprise, for example, a

binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length breast tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports  
5 having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.  
10 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a  
15 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically  
20 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact  
25 time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium  
30 may be readily determined by assaying the level of binding that occurs over a period of

time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second  
5 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of  
10 binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups  
15 and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

20 To determine the presence or absence of a cancer, such as breast cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from  
25 patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,  
30 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity)

that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered  
5 positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or  
10 strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of  
15 bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the  
20 presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a  
25 positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological  
30 sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use  
5 tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within  
10 certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For  
15 example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is  
20 preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on  
25 the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is  
30 then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a

polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above.

10 Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and

15 hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological

20 sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be

25 performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used

30 as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of

reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the  
5 cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such  
10 binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further,  
15 multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

The present invention further provides kits for use within any of the  
20 above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein. Such antibodies or fragments may be provided attached to a support material, as  
25 described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA  
30 encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a

polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

5           The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLE 1

#### ISOLATION AND CHARACTERIZATION OF BREAST

#### 10           TUMOR POLYPEPTIDES

This Example describes the isolation of breast tumor polypeptides from a breast tumor cDNA library.

A cDNA subtraction library containing cDNA from breast tumor subtracted with normal breast cDNA was constructed as follows. Total RNA was  
15   extracted from primary tissues using Trizol reagent (Gibco BRL Life Technologies, Gaithersburg, MD) as described by the manufacturer. The polyA<sup>+</sup> RNA was purified using an oligo(dT) cellulose column according to standard protocols. First strand cDNA was synthesized using the primer supplied in a Clontech PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, CA). The driver DNA consisted of cDNAs from  
20   two normal breast tissues with the tester cDNA being from three primary breast tumors. Double-stranded cDNA was synthesized for both tester and driver, and digested with a combination of endonucleases (MluI, MscI, PvuII, SalI and StuI) which recognize six base pairs DNA. This modification increased the average cDNA size dramatically compared with cDNAs generated according to the protocol of Clontech (Palo Alto,  
25   CA). The digested tester cDNAs were ligated to two different adaptors and the subtraction was performed according to Clontech's protocol. The subtracted cDNAs were subjected to two rounds of PCR amplification, following the manufacturer's protocol. The resulting PCR products were subcloned into the TA cloning vector, pCRII (Invitrogen, San Diego, CA) and transformed into ElectroMax *E. coli* DH10B  
30   cells (Gibco BRL Life, Technologies) by electroporation. DNA was isolated from

independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division (Foster City, CA) Automated Sequencer Model 373A.

Sixty-three distinct cDNA clones were found in the subtracted breast tumor-specific cDNA library. The determined one strand (5' or 3') cDNA sequences for the clones are provided in SEQ ID NO:1-61, 72 and 73, respectively. Comparison of these cDNA sequences with known sequences in the gene bank using the EMBL and GenBank databases (Release 97) revealed no significant homologies to the sequences provided in SEQ ID NO:14, 21, 22, 27, 29, 30, 32, 38, 44, 45, 53, 57, 72 and 73. The sequences of SEQ ID NO: 1, 3, 16, 17, 34, 48, 60 and 61 were found to represent known human genes. The sequences of SEQ ID NO:2, 4, 23, 39 and 50 were found to show some similarity to previously identified non-human genes. The remaining clones (SEQ ID NO:5-13, 15, 18-20, 24-26, 28, 31, 33, 35-37, 40-43, 46, 47, 49, 51, 52, 54-56, 58 and 59) were found to show at least some degree of homology to previously identified expressed sequence tags (ESTs).

Further studies resulted in the isolation of the full-length cDNA sequence for the clone of SEQ ID NO:57 (referred to as B718P). By computer analysis, the full-length sequence was found to contain a putative transmembrane domain at amino acids 137-158. The full-length cDNA sequence of B718P is provided in SEQ ID NO:504, with the cDNA sequence of the open reading frame including stop codon being provided in SEQ ID NO:505 and the cDNA sequence of the open reading frame without stop codon being provided in SEQ ID NO:506. The full-length amino acid sequence of B718P is provided is SEQ ID NO:507. SEQ ID NO:508 represents amino acids 1-158 of B718P, and SEQ ID NO:509 represents amino acids 159-243 of B718P.

To determine mRNA expression levels of the isolated cDNA clones, cDNA clones from the breast subtraction described above were randomly picked and colony PCR amplified. Their mRNA expression levels in breast tumor, normal breast and various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were arrayed onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with

the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. Data was analyzed using Synteni provided GEMTOOLS Software. Of the seventeen cDNA clones examined, those of SEQ ID NO:40, 46, 59 and 73 were found to be over-expressed in breast tumor and expressed at low levels in all normal tissues tested

5 (breast, PBMC, colon, fetal tissue, salivary gland, bone marrow, lung, pancreas, large intestine, spinal cord, adrenal gland, kidney, pancreas, liver, stomach, skeletal muscle, heart, small intestine, skin, brain and human mammary epithelial cells). The clones of SEQ ID NO:41 and 48 were found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested, with the exception of bone marrow. The clone

10 of SEQ ID NO:42 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested except bone marrow and spinal cord. The clone of SEQ ID NO:43 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of spinal cord, heart and small intestine. The clone of SEQ ID NO:51 was found to be over-expressed in breast tumor and

15 expressed at low levels in all other tissues tested with the exception of large intestine. The clone of SEQ ID NO:54 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of PBMC, stomach and small intestine. The clone of SEQ ID NO:56 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of

20 large and small intestine, human mammary epithelia cells and SCID mouse-passaged breast tumor. The clone of SEQ ID NO:60 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of spinal cord and heart. The clone of SEQ ID NO:61 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of small

25 intestine. The clone of SEQ ID NO:72 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of colon and salivary gland.

The results of a Northern blot analysis of the clone SYN18C6 (SEQ ID NO:40) are shown in Fig. 1. A predicted protein sequence encoded by SYN18C6 is

30 provided in SEQ ID NO:62.

Additional cDNA clones that are over-expressed in breast tumor tissue were isolated from breast cDNA subtraction libraries as follows. Breast subtraction libraries were prepared, as described above, by PCR-based subtraction employing pools of breast tumor cDNA as the tester and pools of either normal breast cDNA or cDNA  
5 from other normal tissues as the driver. cDNA clones from breast subtraction were randomly picked and colony PCR amplified and their mRNA expression levels in breast tumor, normal breast and various other normal tissues were determined using the microarray technology described above. Twenty-four distinct cDNA clones were found to be over-expressed in breast tumor and expressed at low levels in all normal tissues  
10 tested (breast, brain, liver, pancreas, lung, salivary gland, stomach, colon, kidney, bone marrow, skeletal muscle, PBMC, heart, small intestine, adrenal gland, spinal cord, large intestine and skin). The determined cDNA sequences for these clones are provided in SEQ ID NO:63-87. Comparison of the sequences of SEQ ID NO:74-87 with those in the gene bank as described above, revealed homology to previously identified human  
15 genes. No significant homologies were found to the sequences of SEQ ID NO:63-73.

Three DNA isoforms for the clone B726P (partial sequence provided in SEQ ID NO:71) were isolated as follows. A radioactive probe was synthesized from B726P by excising B726P DNA from a pT7Blue vector (Novagen) by a BamHI/XbaI restriction digest and using the resulting DNA as the template in a single-stranded PCR  
20 in the presence of [ $\alpha$ -<sup>32</sup>P]dCTP. The sequence of the primer employed for this PCR is provided in SEQ ID NO:177. The resulting radioactive probe was used to probe a directional cDNA library and a random-primed cDNA library made using RNA isolated from breast tumors. Eighty-five clones were identified, excised, purified and sequenced. Of these 85 clones, three were found to each contain a significant open  
25 reading frame. The determined cDNA sequence of the isoform B726P-20 is provided in SEQ ID NO:175, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:176. The determined cDNA sequence of the isoform B726P-74 is provided in SEQ ID NO:178, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:179. The determined cDNA sequence of the isoform  
30 B726P-79 is provided in SEQ ID NO:180, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:181.

Efforts to obtain a full-length clone of B726P using standard techniques led to the isolation of five additional clones that represent additional 5' sequence of B726P. These clones appear to be alternative splice forms of the same gene. The determined cDNA sequences of these clones are provided in SEQ ID NO:464-468, with the predicted amino acid sequences encoded by SEQ ID NO: 464-467 being provided in SEQ ID NO:470-473, respectively. Using standard computer techniques, a 3,681 bp consensus DNA sequence (SEQ ID NO:463) was created that contains two large open reading frames. The downstream ORF encodes the amino acid sequence of SEQ ID NO:176. The predicted amino acid sequence encoded by the upstream ORF is provided in SEQ ID NO:469. Subsequent studies led to the isolation of an additional splice form of B726P that has 184 bp insert relative to the other forms. This 184 bp insert causes a frameshift that brings the down stream and upstream ORFs together into a single ORF that is 1002 aa in length. The determined cDNA sequence of this alternative splice form is disclosed in SEQ ID NO:474, with the corresponding amino acid sequence being provided in SEQ ID NO:475.

Comparison of the cDNA sequence of SEQ ID NO:63 (referred to as B723P) with the sequences in the GeneSeq<sup>TM</sup> DNA database showed matches to 5 DNA sequences (Accession nos. A26456, A37144, A26424, V84525 and T22133), 4 of which appear to represent the full-length sequence of the gene. Three of these sequences encode a 243 amino acid open reading frame (ORF), while one of the DNA sequences (Accession no. A37144) contains an extra C at position 35, resulting in a 278 amino acid ORF. The open reading frame, including stop codon, of the first variant of B723P (referred to as B723P-short) is provided in SEQ ID NO:510, with the open reading frame without stop codon being provided in SEQ ID NO:511. The open reading frame, including stop codon, of the second variant of B723P (referred to as B723P-long) is provided in SEQ ID NO:512, with the open reading frame without stop codon being provided in SEQ ID NO:513. The amino acid sequences of B723P-short and B723P-long are provided in SEQ ID NO:514 and 515, respectively. Computer analysis of these sequences demonstrated the presence of putative transmembrane domains at amino acids 233-252 of the B723P-long ORF and amino acids 198-217 of the B723P-short ORF. SEQ ID NO:516, 518 and 519 represent amino acids 1-197,

198-243 and 218-243, respectively of B723P-short. SEQ ID NO:517 represents amino acids 1-232 of B723P-long.

Further isolation of individual clones that are over-expressed in breast tumor tissue was conducted using cDNA subtraction library techniques described  
5 above. In particular, a cDNA subtraction library containing cDNA from breast tumors subtracted with five other normal human tissue cDNAs (brain, liver, PBMC, pancreas and normal breast) was utilized in this screening. From the original subtraction, one hundred seventy seven clones were selected to be further characterized by DNA sequencing and microarray analysis. Microarray analysis demonstrated that the  
10 sequences in SEQ ID NO:182-251 and 479 were 2 or more fold over-expressed in human breast tumor tissues over normal human tissues. No significant homologies were found for nineteen of these clones, including, SEQ ID NO:185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246 and 479, with the exception of some previously identified expressed sequence tags (ESTs). The  
15 remaining clones share some homology to previously identified genes, specifically SEQ ID NO:181-184, 187-193, 195-198, 200-204, 206, 207, 209, 210, 212, 213, 217, 218, 220, 221, 223-225, 227-231, 233-235, 237-239, 242-244 and 247-251.

One of the cDNA clones isolated by PCR subtraction as described above (SEQ ID NO:476; referred to as B720P) which was shown by microarray to be over-  
20 expressed in breast tumor tissues, was found to be identical to a known keratin gene. The full-length cDNA sequence of the known keratin gene is provided in SEQ ID NO:477, with the corresponding amino acid sequence being provided in SEQ ID NO:478. Primers were generated based on the sequence of SEQ ID NO:477 and used to clone full-length cDNA from mRNA which was obtained from total RNA showing high  
25 expression of B720P in real-time PCR analysis. Products were then cloned and sequenced. The determined full-length cDNA sequence for B720P is provided in SEQ ID NO:484, with the corresponding amino acid sequence being provided in SEQ ID NO:485.

In further studies, a truncated form of B720P (referred to as B720P-tr)  
30 was identified in breast carcinomas. This antigen was cloned from mRNA derived from total breast tumor RNA that showed high expression of B720P-tr in real-time PCR analysis. mRNA was used to generate a pool of cDNA which was then used as a

template to amplify the cDNA corresponding to B720P-tr by PCR. The determined cDNA sequence for B720P-tr is provided in SEQ ID NO:486. B720P-tr has an ORF of 708 base pairs which encodes a 236 amino acid protein (SEQ ID NO:487). The size of the transcript was confirmed by northern analysis.

5                   Of the seventy clones showing over-expression in breast tumor tissues, fifteen demonstrated particularly good expression levels in breast tumor over normal human tissues. The following eleven clones did not show any significant homology to any known genes. Clone 19463.1 (SEQ ID NO:185) was over-expressed in the majority of breast tumors and also in the SCID breast tumors tested (refer to Example 2);  
10 additionally, over-expression was found in a majority of normal breast tissues. Clone 19483.1 (SEQ ID NO:216) was over-expressed in a few breast tumors, with no over-expression in any normal tissues tested. Clone 19470.1 (SEQ ID NO:219) was found to be slightly over-expressed in some breast tumors. Clone 19468.1 (SEQ ID NO:222) was found to be slightly over-expressed in the majority of breast tumors tested. Clone  
15 19505.1 (SEQ ID NO:226) was found to be slightly over-expressed in 50% of breast tumors, as well as in SCID tumor tissues, with some degree of over-expression in found in normal breast. Clone 1509.1 (SEQ ID NO:232) was found to be over-expressed in very few breast tumors, but with a certain degree of over-expression in metastatic breast tumor tissues, as well as no significant over-expression found in normal tissues. Clone  
20 19513.1 (SEQ ID NO:236) was shown to be slightly over-expressed in few breast tumors, with no significant over-expression levels found in normal tissues. Clone 19575.1 (SEQ ID NO:240) showed low level over-expression in some breast tumors and also in normal breast. Clone 19560.1 (SEQ ID NO:241) was over-expressed in 50% of breast tumors tested, as well as in some normal breast tissues. Clone 19583.1  
25 (SEQ ID NO:245) was slightly over-expressed in some breast tumors, with very low levels of over-expression found in normal tissues. Clone 19587.1 (SEQ ID NO:246) showed low level over-expression in some breast tumors and no significant over-expression in normal tissues.

                  Clone 19520.1 (SEQ ID NO:233), showing homology to clone 102D24  
30 on chromosome 11q13.31, was found to be over-expressed in breast tumors and in SCID tumors. Clone 19517.1 (SEQ ID NO:237), showing homology to human PAC 128M19 clone, was found to be slightly over-expressed in the majority of breast tumors

tested. Clone 19392.2 (SEQ ID NO:247), showing homology to human chromosome 17, was shown to be over-expressed in 50% of breast tumors tested. Clone 19399.2 (SEQ ID NO:250), showing homology to human Xp22 BAC GSHB-184P14, was shown to be slightly over-expressed in a limited number of breast tumors tested.

5           In subsequent studies, 64 individual clones were isolated from a subtracted cDNA library containing cDNA from a pool of breast tumors subtracted with cDNA from five normal tissues (brain, liver, PBMC, pancreas and normal breast). The subtracted cDNA library was prepared as described above with the following modification. A combination of five six-base cutters (MluI, MscI, PvuII, SalI and StuI)  
10       was used to digest the cDNA instead of RsaI. This resulted in an increase in the average insert size from 300 bp to 600 bp. The 64 isolated clones were colony PCR amplified and their mRNA expression levels in breast tumor tissue, normal breast and various other normal tissues were examined by microarray technology as described above. The determined cDNA sequences of 11 clones which were found to be over-expressed in  
15       breast tumor tissue are provided in SEQ ID NO:405-415. Comparison of these sequences to those in the public database, as outlined above, revealed homologies between the sequences of SEQ ID NO:408, 411, 413 and 414 and previously isolated ESTs. The sequences of SEQ ID NO:405-407, 409, 410, 412 and 415 were found to show some homology to previously identified sequences.

20           In further studies, a subtracted cDNA library was prepared from cDNA from metastatic breast tumors subtracted with a pool of cDNA from five normal tissues (breast, brain, lung, pancreas and PBMC) using the PCR-subtraction protocol of Clontech, described above. The determined cDNA sequences of 90 clones isolated from this library are provided in SEQ ID NO:316-404. Comparison of these sequences  
25       with those in the public database, as described above, revealed no significant homologies to the sequence of SEQ ID NO:366. The sequences of SEQ ID NO:321-325, 343, 354, 368, 369, 377, 382, 385, 389, 395, 397 and 400 were found to show some homology to previously isolated ESTs. The remaining sequences were found to show homology to previously identified gene sequences.

30           In yet further studies, a subtracted cDNA library (referred to as 2BT) was prepared from cDNA from breast tumors subtracted with a pool of cDNA from six

normal tissues (liver, brain, stomach, small intestine, kidney and heart) using the PCR-subtraction protocol of Clontech, described above. cDNA clones isolated from this subtraction were subjected to DNA microarray analysis as described above and the resulting data subjected to four modified Gemtools analyses. The first analysis  
5 compared 28 breast tumors with 28 non-breast normal tissues. A mean over-expression of at least 2.1 fold was used as a selection cut-off. The second analysis compared 6 metastatic breast tumors with 29 non-breast normal tissues. A mean over-expression of at least 2.5 fold was used as a cut-off. The third and fourth analyses compared 2 early SCID mouse-passaged with 2 late SCID mouse-passaged tumors. A mean over-  
10 expression in the early or late passaged tumors of 2.0 fold or greater was used as a cut-off. In addition, a visual analysis was performed on the microarray data for the 2BT clones. The determined cDNA sequences of 13 clones identified in the visual analysis are provided in SEQ ID NO:427-439. The determined cDNA sequences of 22 clones identified using the modified Gemtools analysis are provided in SEQ ID NO:440-462,  
15 wherein SEQ ID NO:453 and 454 represent two partial, non-overlapping, sequences of the same clone.

Comparison of the clone sequences of SEQ ID NO:436 and 437 (referred to as 263G6 and 262B2) with those in the public databases, as described above, revealed no significant homologies to previously identified sequences. The sequences  
20 of SEQ ID NO:427, 429, 431, 435, 438, 441, 443, 444, 445, 446, 450, 453 and 454 (referred to as 266B4, 266G3, 264B4, 263G1, 262B6, 2BT2-34, 2BT1-77, 2BT1-62, 2BT1-60,61, 2BT1-59, 2BT1-52 and 2BT1-40, respectively) showed some homology to previously isolated expressed sequences tags (ESTs). The sequences of SEQ ID NO:428, 430, 432, 433, 434, 439, 440, 442, 447, 448, 449, 451, 452 and 455-462  
25 (referred to as clones 22892, 22890, 22883, 22882, 22880, 22869, 21374, 21349, 21093, 21091, 21089, 21085, 21084, 21063, 21062, 21060, 21053, 21050, 21036, 21037 and 21048, respectively), showed some homology to gene sequences previously identified in humans.

## EXAMPLE 2

## ISOLATION AND CHARACTERIZATION OF BREAST TUMOR POLYPEPTIDES

## OBTAINED BY PCR-BASED SUBTRACTION USING SCID-PASSAGED TUMOR RNA

Human breast tumor antigens were obtained by PCR-based subtraction  
5 using SCID mouse passaged breast tumor RNA as follows. Human breast tumor was  
implanted in SCID mice and harvested on the first or sixth serial passage, as described  
in Patent Application Serial No. 08/556,659 filed 11/13/95, U.S. Patent No. 5,986,170.  
Genes found to be differentially expressed between early and late passage SCID tumor  
may be stage specific and therefore useful in therapeutic and diagnostic applications.  
10 Total RNA was prepared from snap frozen SCID passaged human breast tumor from  
both the first and sixth passage.

PCR-based subtraction was performed essentially as described above. In  
the first subtraction (referred to as T9), RNA from first passage tumor was subtracted  
from sixth passage tumor RNA to identify more aggressive, later passage-specific  
15 antigens. Of the 64 clones isolated and sequenced from this subtraction, no significant  
homologies were found to 30 of these clones, hereinafter referred to as: 13053, 13057,  
13059, 13065, 13067, 13068, 13071-13073, 13075, 13078, 13079, 13081, 13082,  
13092, 13097, 13101, 13102, 13131, 13133, 13119, 13135, 13139, 13140, 13146-  
13149, and 13151, with the exception of some previously identified expressed sequence  
20 tags (ESTs). The determined cDNA sequences for these clones are provided in SEQ ID  
NO:88-116, respectively. The isolated cDNA sequences of SEQ ID NO:117-140  
showed homology to known genes.

In a second PCR-based subtraction, RNA from sixth passage tumor was  
subtracted from first passage tumor RNA to identify antigens down-regulated over  
25 multiple passages. Of the 36 clones isolated and sequenced, no significant homologies  
were found to nineteen of these clones, hereinafter referred to as: 14376, 14377, 14383,  
14384, 14387, 14392, 14394, 14398, 14401, 14402, 14405, 14409, 14412, 14414-  
14416, 14419, 14426, and 14427, with the exception of some previously identified  
expressed sequence tags (ESTs). The determined cDNA sequences for these clones are  
30 provided in SEQ ID NO:141-159, respectively. The isolated cDNA sequences of SEQ  
ID NO: 160-174 were found to show homology to previously known genes.

Further analysis of human breast tumor antigens through PCR-based subtraction using first and sixth passage SCID tumor RNA was performed. Sixty three clones were found to be differentially expressed by a two or more fold margin, as determined by microarray analysis, i.e., higher expression in early passage tumor over  
5 late passage tumor, or vice versa.. Seventeen of these clones showed no significant homology to any known genes, although some degree of homology with previously identified expressed sequence tags (ESTs) was found, hereinafter referred to as 20266, 20270, 20274, 20276, 20277, 20280, 20281, 20294, 20303, 20310, 20336, 20341, 20941, 20954, 20961, 20965 and 20975 (SEQ ID NO:252-268, respectively). The  
10 remaining clones were found to share some degree of homology to known genes, which are identified in the Brief Description of the Drawings and Sequence Identifiers section above, hereinafter referred to as 20261, 20262, 20265, 20267, 20268, 20271, 20272, 20273, 20278, 20279, 20293, 20300, 20305, 20306, 20307, 20313, 20317, 20318, 20320, 20321, 20322, 20326, 20333, 20335, 20337, 20338, 20340, 20938, 20939,  
15 20940, 20942, 20943, 20944, 20946, 20947, 20948, 20949, 20950, 20951, 20952, 20957, 20959, 20966, 20976, 20977 and 20978. The determined cDNA sequences for these clones are provided in SEQ ID NO:269-314, respectively.

The clones 20310, 20281, 20262, 20280, 20303, 20336, 20270, 20341, 20326 and 20977 (also referred to as B820P, B821P, B822P, B823P, B824P, B825P,  
20 B826P, B827P, B828P and B829P, respectively) were selected for further analysis based on the results obtained with microarray analysis. Specifically, microarray data analysis indicated at least two- to three-fold overexpression of these clones in breast tumor RNA compared to normal tissues tested. Subsequent studies led to the determination of the complete insert sequence for the clones B820P, B821P, B822P,  
25 B823P, B824P, B825P, B826P, B827P, B828P and B829P. These extended cDNA sequences are provided in SEQ ID NO:416-426, respectively.

### EXAMPLE 3

#### SYNTHESIS OF POLYPEPTIDES

30 Polypeptides may be synthesized on an Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-

Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following

5 cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse

10 phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

#### EXAMPLE 4

##### 15 ELICITATION OF BREAST ANTIGEN-SPECIFIC CTL RESPONSES

##### IN HUMAN BLOOD

This Example illustrates the ability of the breast-specific antigen B726P to elicit a cytotoxic T lymphocyte (CTL) response in peripheral blood lymphocytes from normal humans.

20 Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of a normal donor by growth for five days in RPMI medium containing 10% human serum, 30 ng/ml GM-CSF and 30 ng/ml IL-4. Following five days of culture, DC were infected overnight with adenovirus expressing recombinant B726P (downstream ORF; SEQ ID NO:176) at an M.O.I. of 2.5 and

25 matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. CD8 positive cells were enriched for by the depletion of CD4 and CD14-positive cells. Priming cultures were initiated in individual wells of several 96-well plates with the cytokines IL-6 and IL-12. These cultures were restimulated in the presence of IL-2 using autologous fibroblasts treated with IFN-gamma and transduced with B726P and CD80.

30 Following three stimulation cycles, the presence of B726P-specific CTL activity was assessed in IFN-gamma Elispot assays (Lalvani et al., *J. Exp. Med.* 186:859-865, 1997) using IFN-gamma treated autologous fibroblasts transduced to express either B726P or

an irrelevant, control, antigen as antigen presenting cells (APC). Of approximately 96 lines, one line (referred to as 6-2B) was identified that appeared to specifically recognize B726P-transduced APC but not control antigen-transduced APC. This microculture was cloned using standard protocols. B726P-specific CTL were identified  
5 by Elispot analysis and expanded for further analysis. These CTL clones were demonstrated to recognize B726P-expressing fibroblasts, but not the control antigen MART-1, using chromium-51 release assays. Furthermore, using a panel of allogeneic fibroblasts transduced with B726P in antibody blocking assays, the HLA restriction element for these B726P-specific CTL was identified as HLA-B\*1501.

10 In order to define more accurately the location of the epitope recognized by the B726P-specific CTL clones, a deletion construct comprising only the N-terminal half (a.a. 1-129) of B726P (referred to as B726Pdelta3') was constructed in the pBIB retroviral expression plasmid. This plasmid, as well as other plasmids containing B726P, were transfected into COS-7 cells either alone or in combination with a plasmid  
15 expressing HLA-B\*1501. Approximately 48 hours after transfection, a B726P-specific CTL clone (1-9B) was added at approximately  $10^4$  cells per well. The cells were harvested the next day and the amount of IFN-gamma released was measured by ELISA. The CTL responded above background (EGFP) to COS-7 cells that had been transfected with both B726P and HLA-B\*1501. There was no response above  
20 background to COS-7 cells that had been transfected with either B726P or HLA-B\*1501 alone. Importantly, a higher response was seen with COS-7 cells that had been transfected with both HLA-B\*1501 and B726Pdelta3'. This result indicated that the epitope was likely to be located in the N-terminal region (a.a. 1-129) of B726P. This region was examined and amino acid sequences that corresponded to the HLA-B\*1501  
25 peptide binding motif (*J. Immunol.*1999,162:7277-84) were identified and synthesized. These peptides were pulsed at 10 ug/ml onto autologous B-LCL overnight. The next day, the cells were washed and the ability of the cells to stimulate the B726P-specific CTL clone 1-9B was assayed in a IFN-gamma ELISPOT assay. Of the eleven peptides tested, only one peptide, having the amino acid sequence SLTKRASQY (a.a. 76-84 of  
30 B726P; SEQ ID NO: 488) was recognized by the CTL clone. This result identifies this peptide as being a naturally-processed epitope recognized by this B726P-specific CTL clone.

In further studies, a panel of breast tumor cell lines obtained from the American Type Culture Collection (Manassas, VA), was analyzed using real time PCR to determine their B726P message level. The cell line that expressed the highest level of B726P (referred to as HTB21) and a line that expressed no B726P (referred to as HTB132) were transduced with HLA-B\*1501. These cell lines were grown up and analyzed using FACS to determine their B1501 expression. The line HTB 21 was found to endogenously express B1501. To determine if clone 1-9A would recognize the tumor cell line HTB21, an IFN-gamma ELISPOT assay was performed using 20,000 T cells, low dose IL-2 (5 ug/ml), and 20,000 of the following targets: autologous B726P or Mart-1 fibroblasts, untransduced or B1501-transduced HTB21; or untransduced or B1501-transduced HTB132. These were incubated overnight and the assay was developed the next day. The results of this assay are shown in Figure 2. These studies demonstrate that B726P-specific CTL can recognize and lyse breast tumor cells expressing B726P.

#### EXAMPLE 5

##### IDENTIFICATION OF IMMUNOGENIC CD4 T CELL EPITOPES IN BREAST ANTIGENS

Immunogenic CD4 T cell epitopes derived from the breast antigen B726P were identified as follows.

A total of thirty-five 20-mer peptides overlapping by 12 amino acids and derived from the downstream ORF of B726P (corresponding to amino acids 1-317 of SEQ ID NO:176) were generated by standard procedure. Dendritic cells (DC) were derived from PBMC of a normal male donor using GMCSF and IL-4 by standard protocol. Purified CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection of PBMCs. DC were pulsed overnight with pools of the 20-mer peptides, with each peptide at an individual concentration of 0.5 micrograms/mL. Pulsed DC were washed and plated at 10,000 cells/well of 96-well U bottom plates, and purified CD4 T cells were added at 100,000 cells/well. Cultures were supplemented with 10 ng/mL IL-6 and 5 ng/mL IL-12 and incubated at 37 °C. Cultures were restimulated as above on a weekly basis using DC made and pulsed as above as the antigen presenting cell, supplemented with 10 u/mL IL-2 and 5 ng/mL IL-7. Following three *in vitro* stimulation cycles (the initial priming + two restimulations),

cell lines (each corresponding to one well) were tested for specific proliferation and cytokine production in response to the stimulating pool versus an irrelevant pool of peptides derived from unrelated antigens. A number of individual CD4 T cell lines (36/672 by IFN-gamma and 64/672 by proliferation) demonstrated significant cytokine release (IFN-gamma) and proliferation in response to the B726P peptide pools but not to the control peptide pool. Twenty-five of these T cell lines were restimulated on the appropriate pool of B726P peptides and reassayed on autologous DC pulsed with either the individual peptides or recombinant B726P protein made in *E. coli*. Approximately 14 immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these 14 peptides are provided in SEQ ID NO:534 - 547, with the corresponding DNA sequences being provided in SEQ ID NO:520-533, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide but some could be mapped to more than one peptide in each pool. Thirteen of the fifteen T cell lines recognized the recombinant B726P protein. These results demonstrate that 13 of the 14 peptide sequences (SEQ ID NO:534-542 and 544-547) may be naturally processed CD4 epitopes of the B726P protein.

#### EXAMPLE 6

##### 20 PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST BREAST TUMOR ANTIGEN B726P

Polyclonal antibodies against both the downstream (SEQ ID NO:176) and upstream (SEQ ID NO:469) ORF of the breast tumor antigen B726P were prepared as follows.

25 The downstream or upstream ORF of B726P expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37 °C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, 30 the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate

buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then  
5 centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine  
10 HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer.  
15 The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin, such as HiPrepQ (Biorad), was equilibrated with the appropriate buffer and the pooled fractions  
20 from above were loaded onto the column. Antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The protein was then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for  
25 immunization.

Four hundred micrograms of the B726P antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by  
30 incubating the blood at 4 °C for 12-24 hours followed by centrifugation.

Ninety-six well plates were coated with B726P antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250 Microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 min. Plates were again washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H<sub>2</sub>SO<sub>4</sub> and read immediately at 450 nm. All the polyclonal antibodies showed immunoreactivity to the appropriate B726P antigen.

**B) Preparation of polyclonal antibodies against B709P and B720P**

The breast antigens B709P (SEQ ID NO: 62) and B720P (SEQ ID NO: 485) expressed in an *E. coli* recombinant expression system were grown overnight in LB Broth with the appropriate antibiotics at 37°C in a shaking incubator. Ten ml of the overnight culture was added to 500 ml of 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the optical density (at 560 nanometers) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, the mixture was run through a French Press at a pressure of 16,000 psi. The cells were centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine

HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature (RT) with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialled after filtration through a 0.22-micron filter and frozen until needed for immunization.

Four hundred micrograms of antigen was combined with 100 micrograms of muramyl dipeptide (MDP). An equal volume of Incomplete Freund's Adjuvant (IFA) was added and mixed, and the mixture was injected into a rabbit. The rabbit was boosted with 100 micrograms of antigen mixed with an equal volume of IFA every four weeks. The animal was bled seven days following each boost. Sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

The reactivity of the polyclonal antibodies to recombinant antigen (B709P or B720P) was determined by ELISA as follows. Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) at 4°C for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at RT for 2 hrs. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera were diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at RT for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at RT for 30 min. Plates were washed as described above and 100 microliters of TMB Microwell Peroxidase Substrate was added to each well. Following a 15-

minute incubation in the dark at RT, the colorimetric reaction was stopped with 100 microliters of 1N H<sub>2</sub>SO<sub>4</sub> and read immediately at 450 nm. The polyclonal antibodies showed immunoreactivity to the appropriate antigen.

5

## EXAMPLE 7

## PROTEIN EXPRESSION OF BREAST TUMOR ANTIGENS

The downstream ORF of B726P (SEQ ID NO:176), together with a C-terminal 6X His Tag, was expressed in insect cells using the baculovirus expression system as follows.

- 10           The cDNA for the full-length downstream ORF of B726P was PCR amplified using the primers of SEQ ID NO:480 and 481. The PCR product with the expected size was recovered from agarose gel, restriction digested with EcoRI and Hind II, and ligated into the transfer plasmid pFastBac1, which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing.
- 15   The recombinant transfer plasmid pFBB726P was used to make recombinant bacmid DNA and virus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies, Gaithersburg, MD). High Five cells were infected with the recombinant virus BVB726P to produce protein. The cDNA and amino acid sequences of the expressed B726P recombinant protein are provided in SEQ ID NO:482 and 483,
- 20   respectively.

## EXAMPLE 8

GENERATION OF CONSTRUCTS FOR PROTEIN EXPRESSION OF B726P IN *E. COLI*

- Three different open reading frames (ORFs) of B726P were subcloned
- 25   into pPDM, a modified pET28 vector for expression in *E. coli*.

**Construct for the expression of B726P Upstream ORF in *E. coli***  
**(cDNA: SEQ ID NO:549; amino acid: SEQ ID NO:552):**

The partial B726P upstream ORF (A) from clone 23113 was PCR amplified with the following primers:

- 30           PDM-416 (SEQ ID NO:554) 5' gtcggctccatgagtcgccgcaaaag 3' Tm 63°C.

PDM-431 (SEQ ID NO:555) 5' cgagaattcaataacttaagaagaccatctttaccag 3'  
T<sub>m</sub> 61°C.

The amplification conditions were as follows 10 µl 10X Pfu buffer, 1 µl  
10 µM dNTPs, 2 µl 10 µM each oligo, 83 µl sterile water, 1.5 µl Pfu DNA polymerase  
5 (Stratagene, La Jolla, CA), 1 µl PCR 23113. The reaction was first denatured for 2  
minutes at 96°C, followed by 40 cycles of 96°C for 20 seconds, 62°C for 15 seconds,  
and extension at 72°C for 2 minutes. This was followed by a final extension of 72°C for  
4 minutes.

The second partial B726P upstream ORF (B) from clone 19310 was PCR  
10 amplified with the following primers:

PDM-432 (SEQ ID NO:556) 5' cataagcttaaggctaactgcggaatgaaag 3' T<sub>m</sub>  
63°C.

PDM-427 (SEQ ID NO:557) 5' cccgcagaattcaacatgcaatttcatgtaagag 3'  
T<sub>m</sub> 62°C.

15 The amplification and cycling conditions were as described above. The  
first PCR product was digested with EcoRI and cloned into pPDM His (a modified  
pET28 vector) that had been digested with EcoRI and Eco72I. The second PCR product  
was digested with BfrI and EcoRI and cloned into the resulting construct: pPDM B726P  
UP-A-5 at the EcoRI and BfrI sites. The construct (pPDM B726P Up-4) was confirmed  
20 to be correct through sequence analysis and transformed into BL21 (DE3) pLys S and  
BL21 CodonPlus RIL (DE3) cells. Protein expression was confirmed by Coomassie  
stained SDS-PAGE and N-terminal protein sequence analysis.

**Construct for B726P D-ORF expression in *E. coli* (cDNA: SEQ ID  
NO:550; amino acid: SEQ ID NO:551):**

25 The B726P D-ORF was PCR amplified with the following primers:

PDM-290 (SEQ ID NO:558) 5' ctaaagccggcacaagagctctgc 3' T<sub>m</sub> 61°C

PDM-291 (SEQ ID NO:559) 5' cgcgagaattctattatataacttctgttctgc 3'

T<sub>m</sub>61°C

The reaction conditions were as described. The cycling conditions were  
30 altered slightly in that the annealing temperature was lowered to 61°C from 62°C and  
was held for 15 seconds. The extension time was also increased to 2 minutes and 15

seconds. The PCR product was digested with NaeI and EcoRI and cloned into pPDM His which has been digested with Eco72I and EcoRI. Construct was confirmed by sequencing and then transformed into BL21 (DE3) pLys S cells (Novagen, Madison, WI). Protein expression was confirmed by Coomassie stained SDS-PAGE and N-terminal protein sequence analysis.

**Construct for B726P Combined ORF expression in *E. coli* (cDNA: SEQ ID NO:548; amino acid: SEQ ID NO:553):**

The B726P C-1 coding region was PCR amplified including the 183bp insert, with the following primers:

10 PDM-750 (SEQ ID NO:560) 5' ggggaattgtgagcggataacaattc 3' Tm 58°C  
PDM-752 (SEQ ID NO:561) 5' cgtagaattcaacctgattaaattactttctacac 3'  
Tm 59°C

The B726P Downstream ORF was PCR amplified with the following primers:

15 PDM-753 (SEQ ID NO:562) 5' gaaagtaatttaaatcaggtttctcacactc 3' Tm  
59°C

PDM-751 (SEQ ID NO:563) 5' gagggccccaagggttatgctag 3' Tm 61°C

The reaction conditions for these PCR reactions were the same as described above. The cycling conditions were as follows: 1<sup>st</sup> PCR: The reaction was  
20 first denatured for 2 minutes at 96°C, followed by 40 cycles of 96°C for 20 seconds, 58°C for 15 seconds, and extension at 72°C for 4 minutes. This was followed by a final extension of 72°C for 4 minutes; 2<sup>nd</sup> PCR: . The reaction was first denatured for 2 minutes at 96°C, followed by 40 cycles of 96°C for 20 seconds, 59°C for 15 seconds, and extension at 72°C for 2 minutes. This was followed by a final extension of 72°C for  
25 4 minutes. The first PCR product was digested with EcoRI and cloned into pPDM His (a modified pET28 vector) at the Eco 72I and EcoRI sites. The construct was confirmed to be correct through sequence analysis. The second PCR product was digested with EcoRI and cloned into pPDM His at the same sites. The resulting constructs pPDM B726P UA-8 and pPDM B726P DA-7 respectively were digested with SmaI and EcoRI.  
30 The pPDM B726P UA-8 construct was used as vector and the insert from the pPDM B726P DA-7 was cloned into this construct successfully. The construct was confirmed

to be correct through sequence analysis and then transformed into BLR (DE3) pLys S and HMS 174 (DE3) pLys S cells (Novagen, Madison, WI). Protein expression was confirmed by Coomassie stained SDS-PAGE and N-terminal protein sequence analysis.

5

## EXAMPLE 9

## ADDITIONAL SEQUENCE IDENTIFIED FOR BREAST TUMOR ANTIGEN B726P BY

## BIOINFORMATIC ANALYSIS

The combined ORF of the breast tumor antigen, B726P (amino acid sequence set forth in SEQ ID NO:475), was used to search public databases. A  
10 sequence essentially identical to the combined ORF with additional N-terminal sequence was identified in the GenBank nonredundant protein database and the cDNA and predicted amino acid sequences are set forth in SEQ ID NO:564 and 565, respectively. The gene is also referred to as NY-BR-1 and was described in described in Cancer Research 61(5):2055-2061, March 1, 2001.

15

## EXAMPLE 10

## ANALYSIS OF B726P EXPRESSION USING IMMUNOHISTOCHEMISTRY

Affinity purified polyclonal antibodies anti-B726Pup (generated against the B726P upstream ORF protein) and anti-B726Pdown (generated against the B726P  
20 downstream ORF) were used to assess B726P protein expression in breast cancer and in a variety of normal tissue sections.

In order to determine which tissues express the breast cancer antigen protein B726P immunohistochemistry (IHC) analysis was performed on a diverse range of tissue sections. Tissue samples were fixed in formalin solution for 12-24 hrs and  
25 embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (either rabbit affinity purified anti-B726Pdown or anti-B726Pup) was added to each section for 25 minutes followed by 25 minute incubation with anti-rabbit  
30 biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish

peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin to visualize cell nuclei. Anti-B726Pup and anti-B726Pdown immunoreactivity was observed in about 30-40% of breast cancer samples analyzed but not observed in a majority of various normal tissues. Anti-B726Pdown and anti-b726Pup also stained roughly the same breast cancer samples. Thus, these data confirm earlier microarray analysis (see Example 1) showing that B726P is overexpressed in breast tumor tissue as compared to normal tissue. Therefore, this antigen may be used in diagnostic and immunotherapeutic applications for breast cancer.

10

## EXAMPLE 11

## GENERATION OF MONOCLONAL ANTIBODIES TO B726P DOWNSTREAM AND UPSTREAM ORFs

Production and purification of protein used for antibody generation.

15 B726 upstream ORF and B726 downstream ORF proteins were expressed in an *E. coli* recombinant expression system (see Example 8). Cells were grown overnight in LB Broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml of 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the optical density (at 560  
20 nanometers) of the culture reached 0.4-0.6 the cells were induced with IPTG (1 mM). Four hours after induction with IPTG the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed.  
25 To break open the *E. coli* cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This  
30 procedure was repeated twice more. The washed inclusion body pellet was solubilized

with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole.

The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen, Valencia, CA) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. This material was then submitted to Quality Control for final release. The release criteria were purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal protein sequence, and endotoxin level as determined by the Limulus (LAL) assay. The proteins were then vialled after filtration through a 0.22-micron filter and the antigens were frozen until needed for immunization.

To generate anti-B726P mouse monoclonal antibodies, mice were immunized IP with 50 micrograms of recombinant B726P upstream ORF and B726P downstream ORF proteins that had been mixed to form an emulsion with an equal volume of Complete Freund's Adjuvant (CFA). Every three weeks animals were injected IP with 50 micrograms of recombinant B726P upstream ORF and B726P downstream ORF that had been mixed with an equal volume of IFA to form an emulsion. After the fourth injection, spleens were isolated and standard hybridoma fusion procedures were used to generate anti-B726P mouse monoclonal antibody hybridomas. Anti-B726P monoclonal antibodies were screened using the ELISA

analysis using the bacterially expressed recombinant B726P upstream ORF and B726P downstream ORF proteins.

A list of the mouse anti-B726P monoclonal antibodies that were generated, as well as their anti-B726P reactivity in an ELISA assay and Western blot are shown in Table 2. The hybridomas were then subcloned and the subclones further tested for reactivity with B726P upstream ORF and B726P downstream ORF proteins. Several monoclonal antibodies showed particularly favorable reactivity: 220A2-21, 220A19-25, 220A94-29, 220A151-33.

For Western blot analysis, recombinant B726P upstream ORF and B726P downstream ORF protein was diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. Protein was transferred to nitrocellulose and probed with each of the anti-B726P hybridoma supernatants. Protein A-HRP was used to visualize the anti-B726P reactive bands by incubation in ECL substrate.

15

TABLE 2: B726PUP AND B726PDOWN MONOCLONAL ANTIBODY REACTIVITY

Anti-B726P mAbs	ELISA			Western Blots	
	B726PDown	B726PUp	L523S	B726Pdown	B726Pup
220A2	+++	+	-	+++	++
220A10	-	-	-	N/A	N/A
220A14	+++	+++	+++	+++	++
220A19	++	-	-	++	+
220A43	+++	+	-	+++	++
220A86	+++	+	-	+++	++
220A94	+++	-	-	++	+/-
220A123	++	-	-	+	-
220A139	+/-	-	-	+	-
220A140	-	-	-	N/A	N/A
220A141	-	-	-	N/A	N/A
220A143	-	-	-	N/A	N/A

220A151	++	-	-	++	-
220A176	+/-	-	-	+	-

## EXAMPLE 12

## IDENTIFICATION OF ADDITIONAL SEQUENCES FOR B726P

Additional 5' sequence was obtained for B726P - this sequence was  
 5 obtained by PCR from 1st strand cDNA prepared from three separate mRNA sources  
 (metastatic breast tumor, breast tumor, normal testis). Disclosed herein are clones that  
 were isolated, each with differences from the expected published sequence of NY-BR-1.

A 1300 bp fragment of B726P otherwise known as NY-BR-1 was PCR  
 amplified from 1st strand cDNA and cloned into pPDM, a modified pET28 vector as  
 10 follows:

The B726P XB coding region (NY-BR-1) was PCR amplified with the  
 following primers

PDM-784 5' cacacaaagaggaagaagaccatc 3' Tm 56°C

PDM-814 5' gattctttgttaggacatgcaatcatc 3' Tm 55°C

15

The following PCR conditions were used: 10µl 10X Herculase buffer,  
 1µl 10mM dNTPs, 2µl 10.µM each oligo, 83µl sterile water, 1.5µl Herculase DNA  
 polymerase (Stratagene, La Jolla, CA), 50 ng DNA. The thermalcycling conditions  
 were as follows:

20

98°C 3 minutes

98°C 40 seconds, 51°C 15 seconds, 72°C 4 minutes, X 10 cycles

98°C 40 seconds, 51°C 15 seconds, 72°C 5 minutes, X 10 cycles

98°C 40 seconds, 51°C 15 seconds, 72°C 6 minutes, X 10 cycles

98°C 40 seconds, 51°C 15 seconds, 72°C 7 minutes, X 10 cycles

25

72°C 10 minutes

The PCR product was ligated into the pPDM vector (a modified pET28)  
 that had been digested with Eco72I and de-phosphorylated. PCR amplification of this  
 gene proved very difficult and required the use of a polymerase lacking proofreading  
 capabilities. However, use of such an enzyme, in this case, Herculase from Stratagene

(La Jolla, CA), led to what is likely PCR errors in the resulting clones. The cDNA sequence of three of the isolated clones containing mutations are disclosed in SEQ ID NO:567-569 with the corresponding amino acid sequences disclosed in SEQ ID NO:572, 571, and 570, respectively.

5 The resulting construct, pPDM B726P XB (clone 83686), was then digested with BglII and the insert which dropped out from the 5' vector BglII site and the internal BglII site at amino acids 390-391 was cloned into the pPDM B726P C-ORF (SEQ ID NO:548) that had been digested with BglII and was de-phosphorylated. This construct, pPDM B726P XC, was then DNA sequenced and showed two nucleotide  
10 changes, which result in two amino acid changes. The cDNA of the full-length clone containing these 2 mutations is disclosed in SEQ ID NO:566 with the corresponding amino acid sequence in SEQ ID NO:573. The full-length expected, published NY-BR-1 is disclosed in SEQ ID NO:564 (cDNA); amino acid SEQ ID NO:565.

### EXAMPLE 13

## ISOLATION OF ADDITIONAL 3' SEQUENCE AND REAL-TIME PCR ANALYSIS OF B726P HOMOLOG NY-BR1.1

A sequence homolog to the breast candidate B726P, called NY-BR-1.1, was identified and published in Cancer Research 61(5):2055-2061; March 1, 2001. The NY-BR-1.1 gene, thought to be located on chromosome 9 based on 100% sequence identity to genomic sequence from chromosome 9, was shown to be expressed as mRNA in breast tumors as well as in normal brain. However, the published sequence was lacking 3' sequence. Published incomplete sequence for NY-BR-1.1 is represented by GenBank accession number AF269088. A recent BlastN search of the GenBank High Throughput Genomic Sequence database using Ny-Br-1.1 as a query sequence showed a 100% match to the working draft sequence of chromosome 9 (GenBank accession number AL359312), yielding further 3' DNA sequence for Ny-Br-1.1. The compilation of the Ny-Br-1.1 sequence with the additional 3' sequence from chromosome 9 yielded a 3720 bp ORF sequence (SEQ ID NO:576) which encodes a 1240 amino acid protein sequence (SEQ ID NO:577).

Real time PCR primers were designed to a unique region of NY-BR-1.1 to distinguish its mRNA expression profile from B726P. This experiment represents relative values, as it was done without template. The first-strand cDNA used in the quantitative real-time PCR was synthesized from 20 µg of total RNA that was treated with DNase I (Amplification Grade, Gibco BRL Life Technology, Gaithersburg, MD), using Superscript Reverse Transcriptase (RT) (Gibco BRL Life Technology, Gaithersburg, MD). Real-time PCR was performed with a GeneAmp<sup>TM</sup> 5700 sequence detection system (PE Biosystems, Foster City, CA). The 5700 system uses SYBR<sup>TM</sup> green, a fluorescent dye that only intercalates into double stranded DNA, and a set of gene-specific forward and reverse primers. The increase in fluorescence was monitored during the whole amplification process. The optimal concentration of primers was determined using a checkerboard approach and a pool of cDNAs from tumors was used in this process. The PCR reaction was performed in 25 µl volumes that included 2.5 µl of SYBR green buffer, 2 µl of cDNA template and 2.5 µl each of the forward and reverse primers for the gene of interest. The cDNAs used for quantitative real time PCR reactions were diluted 1:10 for each gene of interest and 1:100 for the β-actin control. Levels of mRNA were expressed relative to ureter where NY-BR-1.1 expression was not observed when compared to the β-actin control.

The real time PCR results show that mRNA expression for NY-BR-1.1 is present in breast tumors as well as in normal adrenal gland, brain, retina and testis.

#### EXAMPLE 14

##### CHARACTERIZATION OF B726P MONOCLONAL AND PURIFIED POLYCLONAL ANTIBODY

##### EPITOPES

Mouse monoclonal antibodies and rabbit polyclonal sera were raised against *E. coli* derived B726P recombinant protein and tested by ELISA as described in further detail below, for antibody epitope recognition against overlapping 20 mer peptides that correspond to the amino acid sequence of the downstream ORF of B726P (B726P dORF, set forth in SEQ ID NO:176, encoded by SEQ ID NO:175). Numerous peptides were recognized by the monoclonal and polyclonal antibodies. The

corresponding amino acid sequences of these peptide antibody epitopes are summarized in Table 3 and are set forth in SEQ ID NO:578-593.

ELISA ANALYSIS: B726P recombinant protein and peptides were coated onto 96 well ELISA plate: 50ul/well at 2 ug/ml for 20 hrs at 4C. Plates were then washed 5 times with PBS + 0.1% Tween 20 and blocked with PBS + 1% BSA for 2 hr. Affinity purified B726P polyclonal antibodies were then added to the wells at 1ug/ml and B726P monoclonal supernatants were added neat (220A43 and 220A86 were diluted 1/60 and 1/20 respectively). Plates were incubated at room temperature for 30 minutes and then washed again as above, followed by the addition of 50ul/well donkey anti-mouse-Ig-HRP antibody for 30 minutes at room temperature. Plates were washed, then developed by the addition of 100ul/well of TMB substrate. The reaction was incubated 15 minutes in the dark at room temperature and then stopped by the addition of 100ul/well of 1N H<sub>2</sub>SO<sub>4</sub>. Plates were read at OD450 in an automated plate reader. Peptides with OD450 readings three times background or above were considered to be positively recognized by the corresponding antibody.

Table 3:Peptides recognized by B726P Antibodies

	B726P Monoclonal Supernatant						B726P Purified Polyclonal
	220A2.1	220A19.1	220A94.1	220A151.1	220A43	220A86	(1ug/ml)
B726P peptides (amino acids)	289- 308	225- 244, 232- 252	73- 252	145- 164, 153- 172	232- 252	145- 164, 153- 172	1-20, 9-28, 17- 36, 24-44, 97- 116, 105-124, 113-132, 121- 140, 129-148, 137-156

## EXAMPLE 15

## ANALYSIS OF AUTOANTIBODIES TO B726P IN BREAST CANCER SERA AND EPITOPE

## MAPPING OF THE ANTIGENIC SITES

Specific B726P peptide epitopes were identified that react with  
5 autoantibodies in the serum of breast cancer patients. Thirty-three overlapping peptides  
were synthesized spanning the entire B726P protein. These 33 peptides were tested in  
ELISAs to evaluate which epitopes reacted with breast cancer sera. Reactive epitopes  
were identified throughout the molecule and a total of 16/74 sera samples from breast  
cancer patients had reactivity with one or more peptides.

10 Thirty-one overlapping synthetic peptides spanning the entire B726P  
downstream ORF sequence (amino acid sequence set forth in SEQ ID NO:176) were  
synthesized and 30 of these were tested in ELISA with sera from breast cancer patients  
as well as control sera. The amino acid sequences of the 31 overlapping peptides of the  
B726P downstream ORF are set forth in SEQ ID NO:594-624. Three additional  
15 peptides of B726P, set forth in SEQ ID NO:625-627 were also tested. Several peptides  
throughout the molecule showed reactivity, in particular peptide #2735 (amino acids 31-  
50; SEQ ID NO:597), peptide #2747 (amino acids 151-170; SEQ ID NO:609), peptide  
#2750 (amino acids 181-200; SEQ ID NO:612), peptide #2753 (amino acids 211-230;  
SEQ ID NO:615), and peptide #2766 (amino acids 231-250; SEQ ID NO:617). A total  
20 of 16/74 breast cancer sera were reactive with at least one peptide.

B726P antibody epitopes were also mapped using rabbit antisera  
generated against the B726P downstream ORF (SEQ ID NO:176). The epitopes  
identified using the rabbit antisera were as follows: peptide #2732 (amino acids 1-20;  
SEQ ID NO:594), peptide # 2733 (amino acids 11-30; SEQ ID NO:595), peptide #2742  
25 (amino acids 101-120; SEQ ID NO:604), peptide #2743 (amino acids 111-130; SEQ ID  
NO:605), peptide #2744 (amino acids 121-140; SEQ ID NO:606), peptide #2745  
(amino acids 130-151; SEQ ID NO:607), peptide #2751 (amino acids 191-210; SEQ ID  
NO:613), and peptide #2753 (amino acid 211-230; SEQ ID NO:615). Some low level  
reactivity was observed for peptide #2772 (amino acids 291-310; SEQ ID NO:623) and  
30 peptide #2773 (amino acids 298-317; SEQ ID NO:624).

The above results confirm that B726P can be used alone or in combination with other breast tumor antigens as a vaccine target. Additionally, these results show that detection of antibodies to B726P can be used as a diagnostic indicator of breast cancer either alone or in combination with detection of antibodies to other  
5 antigens (*e.g.* Her-2/Neu or other antigens known to be expressed in breast cancer tissue).

#### EXAMPLE 16

##### IMMUNOHISTOCHEMICAL ANALYSIS OF B726P EXPRESSION IN METASTATIC BREAST

##### 10 CANCER

Affinity purified polyclonal antibodies anti-B726Pdown (generated against the B726P downstream ORF) were used to assess B726P protein expression in metastatic breast cancer samples.

In order to determine which tissues express the breast cancer antigen  
15 protein B726P immunohistochemistry (IHC) analysis was performed on a diverse range of tissue sections. Tissue samples were fixed in formalin solution for 12-24 hrs and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes.  
20 Primary antibody (rabbit affinity purified anti-B726Pdown) was added to each section for 25 minutes followed by 25 minute incubation with anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize antigen expression. Slides  
25 were counterstained with hematoxylin to visualize cell nuclei.

Anti-B726Pdown immunoreactivity was observed in 7 of 10 metastatic breast cancer samples analyzed but not observed in various normal tissues including normal breast. Thus, these data confirm earlier microarray analysis (see Example 1) showing that B726P is overexpressed in breast tumor tissue as compared to normal  
30 tissue. Therefore, this antigen may be used in diagnostic and immunotherapeutic applications for breast cancer.

## EXAMPLE 17

ANALYSIS OF B726P EXPRESSION USING IMMUNOPRECIPITATION AND WESTERN BLOT  
ANALYSIS

Affinity purified polyclonal antibodies generated against the B726P  
5 downstream ORF protein set forth in SEQ ID NO:176 (anti-B726Pdown) were used to  
assess the protein expression of the combined ORF of B726P in breast cancer cell lines  
as compared to normal cells as described below. Since the combined ORF includes  
both the upstream and downstream ORFs, the antibodies generated against the  
downstream ORF crossreact with the combined ORF polypeptide as set forth in SEQ ID  
10 NO:475.

Cells were lysed in 1% Triton lysis buffer on ice for 10 minutes. Lysates  
were centrifuge at 15000 rpm and supernatant was saved for immunoprecipitation  
(IP)/Western analysis. 2 µg of anti-B726down polyclonal antibody was added to the  
supernatant and rocked overnight at 4°C. 20 µl of protein G bead slurry was added and  
15 incubated for 1 hour. Beads were then washed 3 times with 1 ml of lysis buffer. LDS  
sample buffer and β-mercaptoethanol were added and the samples were heated for 5  
min at 95°C. Samples were size fractionated by gel electrophoresis, transferred to  
nitrocellulose and Western blotted with the mouse anti-B726down monoclonal antibody  
A2.1.

20 <sup>35</sup>S methionine labeling/IP analysis was carried out as follows: Cells  
were grown in 10% Fetal Bovine Serum (FBS) media to desired density. Cells were  
then starved with DMEM lacking methionine containing 0.1% FBS media for 10 – 15  
minutes. FBS was added to a final concentration of 10% along with <sup>35</sup>S-Methionine  
translabel (300 µCi – 1 mCi). After incubating for 3 –4 hours the cells were harvested,  
25 washed, and lysed. B726P was immunoprecipitated as described above and samples  
were size fractionated by gel electrophoresis before being exposed to autoradiography  
film.

The results from the above described experiments showed that the full  
length 148 kDa form (also called NYBR1), the 110 kDa combined ORF form, and the  
30 35 kDa downstream ORF form are all expressed in breast tumor cell lines HTB21 and  
BT474 but not in the SKBR3 normal breast cell line. Therefore, these results confirm

that these forms of the B726P protein are expressed in breast tumor cell lines and not in normal cells.

U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications  
5 referred to in this specification and/or listed in the Application Data Sheet, are incorporated herein by reference in their entirety.

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the  
10 invention. Accordingly, the invention is not limited except as by the appended claims.

## CLAIMS

What is Claimed:

1. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides comprising an amino acid sequence set forth in any one of SEQ ID NOs:537, 534-536, and 538-547;

(b) sequences having at least 70% identity to an amino acid sequence set forth in SEQ ID NOs:537, 534-536, and 538-547;

(c) sequences having at least 90% identity to an amino acid sequence set forth in SEQ ID NOs:537, 534-536, and 538-547;

(d) polynucleotides comprising any one of the sequences set forth in SEQ ID NOs:530, 520-529, and 531-533;

(e) sequences having at least 70% identity to a polynucleotide set forth in SEQ ID NOs:530, 520-529, and 531-533;

(f) sequences having at least 90% identity to a polynucleotide set forth in SEQ ID NOs:530, 520-529, and 531-533; and

(g) antigen-presenting cells that express a polynucleotide according to (d), (e), or (f);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

2. An isolated T cell population, comprising T cells prepared according to the method of claim 1.

3. A method for the treatment of breast cancer in a patient, comprising the steps of:

(i) incubating CD4+ and/or CD8+ T cells isolated from a patient, such that T cell proliferate, with at least one component selected from the group consisting of:

(a) polypeptides comprising an amino acid sequence set forth in any one of SEQ ID NOs:537, 534-536, and 538-547;

(b) sequences having at least 70% identity to an amino acid sequence set forth in SEQ ID NOs:537, 534-536, and 538-547;

(c) sequences having at least 90% identity to an amino acid sequence set forth in SEQ ID NOs:537, 534-536, and 538-547;

(d) polynucleotides comprising any one of the sequences set forth in SEQ ID NOs:530, 520-529, and 531-533;

(e) sequences having at least 70% identity to a polynucleotide set forth in SEQ ID NOs:530, 520-529, and 531-533;

(f) sequences having at least 90% identity to a polynucleotide set forth in SEQ ID NOs:530, 520-529, and 531-533; and

(g) antigen-presenting cells that express a polynucleotide according to (d), (e), or (f);

(ii) administering to the patient an effective amount of the proliferated T cells, and

thereby inhibiting the development of a cancer in the patient.

4. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NOs:530, 520-529, and 531-533;

(b) complements of the sequences provided in SEQ ID NOs:530, 520-529, and 531-533;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NOs:530, 520-529, and 531-533;

- (d) sequences that hybridize to a sequence provided in SEQ ID NOs:530, 520-529, and 531-533, under highly stringent conditions;
- (e) sequences having at least 75% identity to a sequence of SEQ ID NOs:530, 520-529, and 531-533;
- (f) sequences having at least 90% identity to a sequence of SEQ ID NOs:530, 520-529, and 531-533; and
- (g) degenerate variants of a sequence provided in SEQ ID NOs:530, 520-529, and 531-533.

5. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) sequences encoded by a polynucleotide of claim 4; and
- (b) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 4; and
- (c) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 4;
- (d) sequences set forth in SEQ ID NOs:537, 534-536, and 538-547;
- (e) sequences having at least 70% identity to a sequence set forth in SEQ ID NOs:537, 534-536, and 538-547; and
- (f) sequences having at least 90% identity to a sequence set forth in SEQ ID NOs:537, 534-536, and 538-547.

6. An expression vector comprising a polynucleotide of claim 4 operably linked to an expression control sequence.

7. A host cell transformed or transfected with an expression vector according to claim 6.

8. A method for detecting the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 5;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

9. A fusion protein comprising at least one polypeptide according to claim 5.

10. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 5;
- (b) polynucleotides according to claim 4;
- (c) fusion proteins according to claim 9;
- (d) T cell populations according to claim 2; and
- (e) antigen presenting cells that express a polypeptide according to claim 7.

11. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 10.

12. A method for the treatment of a breast cancer in a patient, comprising administering to the patient a composition of claim 10.

1/2

# SYN18C6 NORTHERN BLOT

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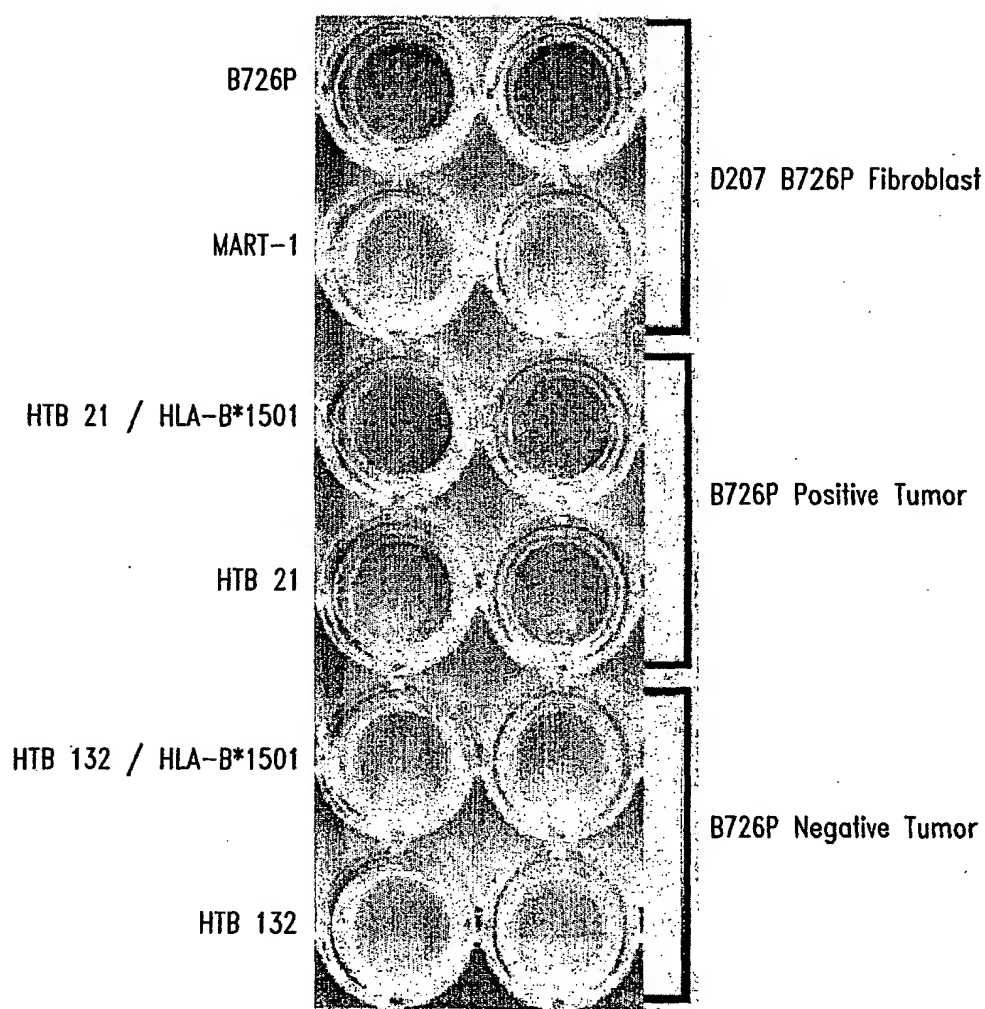
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*Fig. 1*

2/2

D207 B726P-specific CTL Clone 1-9 recognize HTB 21  
a breast tumor cell line that expresses HLA-B\*1501 and B726P

*Fig. 2*

## SEQUENCE LISTING

<110> Houghton, Raymond L.  
 Sleath, Paul R.  
 Persing, David H.  
 Jiang, Yuqiu  
 Dillon, Davin C.  
 Mitcham, Jennifer L.  
 Xu, Jiangchun  
 Harlocker, Susan L.  
 Hepler, William T.  
 Henderson, Robert A.  
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 Vedvick, Thomas S.  
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<120> COMPOSITIONS AND METHODS FOR THE THERAPY  
 AND DIAGNOSIS OF BREAST CANCER

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&lt;210&gt; 23

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 23

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&lt;210&gt; 24

&lt;211&gt; 214

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 24

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tccacaaata	ctgaggtata	gcctgcatgc	cactaaaaat	aacaaagggt	tcaggggtgg	180
aaacattgtc	caccacactg	tcatgacat	cttt			214

&lt;210&gt; 25

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 25

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agctcatggg	tggaggagtc	tccaccagag	ggaggctcag	gggactgggt	gggccaggga	240
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 <212> DNA  
 <213> Homo sapien

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 gccaggatct gggcctgttt cttcccttct gccacattga tggccgactc tcgggtcccc 240  
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 t 301

<210> 27  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 27  
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 cttggtgcaa attaattgcc tgggtactcac agtcagtggt taacaggcaa taatggtgtg 240  
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<210> 28  
 <211> 286  
 <212> DNA  
 <213> Homo sapien

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 gtcccttggt caccaaatgg tcaaagggtc aaagatcggg ggaggtcagg gggtaacgca 180  
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<210> 29  
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 <212> DNA  
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<400> 29  
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 acaggttaca tcattccaat tttgccttgg gtttgaagag tctctcatgg tggcacagtc 180  
 ctccagggtg gctatgttgt tgggctcccc tacatcccag aagctcagag actttgtcaa 240  
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 <212> DNA  
 <213> Homo sapien

<400> 30

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ccaggcaatt aatttgcacc aagaaagtgg aggggtattat cagatattgc aatctgtaca	180
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&lt;210&gt; 31

&lt;211&gt; 141

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 31

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ccgggggaag ggagaggga c	141

&lt;210&gt; 32

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 32

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catccaccta cataaccaac atagatgtga ggtccactgc actgatagcc agactgcctg	180
gggtaaacct tttcagggag g	201

&lt;210&gt; 33

&lt;211&gt; 181

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 33

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gactaaactt caagtcacag acttttatgt gacagattgg agcaggggtt gttatgcatg	120
tagagaacc aaactaatat attaaacagg atagaaacag gctgtctggg tgaaatggtt	180
c	181

&lt;210&gt; 34

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 34

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catttctcct caccacgggg tcgcttgta gctccaagaa ccagtctggc cccactgaga	120
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&lt;210&gt; 35

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 35

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agctttaaca cgtgtaatct gcagtcctta acagtggcgt aattgtacgt acctgttggt	120
tttcagtttg tttttcacct ataataaatt gtaaaaaaaa acatacttgt ggggtctgat	180

agcaaacata gaaatgatgt atattgtttt ttgttatcta tttattttca tcaatacagt 240  
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gtgaaacaca caagccaatc cggaactgct gtgcgaaaga taaaatcgag aaaggcaagg 180  
tttcggtagg aggacgcgat g 201

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<211> 121  
<212> DNA  
<213> Homo sapien

<400> 37  
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c 121

<210> 38  
<211> 200  
<212> DNA  
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<400> 38  
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gataacacca cacatagaac attataatta cacacaaatt tatggtaaaa gaattaatat 180  
gctgtctggt gctgctgtta 200

<210> 39  
<211> 760  
<212> DNA  
<213> Homo sapien

<400> 39  
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ttttaacagt gatcaaatta ttatttcgaa gttaatcgtt cccttggtgg ctgcatacac 180  
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<210> 40  
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<212> DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 40

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ggtttatogt gactttttct tcttgtttac ttttcgctag gaaggggagt tgtaggggca	180
gattcaggta ttggaatagg aaaattacgt ctaaaccatg gaaatcttgg aaatggaatt	240
ggtggaagtg ggcgaaatgg atatgggtaa gggaacacaa aaaaccctga agctaattca	300
tcgctgtcac tgatacttct tttttctcgt tcctggctct gagagactgg gaaaccaaca	360
gccactgcc aagatggctgt gatcaggagg agaactttct tcactctcaa cgtttcagtc	420
agttctttct ctcacctcgg ccgcgaccac gc	452

&lt;210&gt; 41

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 41

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cagacctgcc cgggcg	676

&lt;210&gt; 42

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 42

agcgtggtcg cggccgagggt ttggccggga gcctgatcac ctgccctgct gagtcccagg	60
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&lt;210&gt; 43

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 43

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aatgcatttg taaagggtct gccagatagg aagatgctag ttatggattt acaagggtgt	300
taaggctgta agagtctaaa acctacagt aatcacaatg catttaccct cactgacttg	360

gacataagtg aaaactagcc cgaagtctct ttttcaaatt acttacag 408

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<212> DNA  
<213> Homo sapien

<400> 44  
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<212> DNA  
<213> Homo sapien

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<210> 46  
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<212> DNA  
<213> Homo sapien

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<210> 47  
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<212> DNA  
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<212> DNA  
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 <213> Homo sapien

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<210> 50  
 <211> 271  
 <212> DNA  
 <213> Homo sapien

<400> 50						
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<210> 51  
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 <212> DNA  
 <213> Homo sapien

<400> 51						
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 <213> Homo sapien

<400> 52						
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<210> 53  
 <211> 493  
 <212> DNA  
 <213> Homo sapien

<400> 53  
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 <213> Homo sapien

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 gactttctct ctggagatac ctttttgaat atacaatggc cttggctcac taggtttaa 240  
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<210> 55  
 <211> 281  
 <212> DNA  
 <213> Homo sapien

<400> 55  
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<210> 56  
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 <212> DNA  
 <213> Homo sapien

<400> 56  
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 ggggtgttgg gagagactgt gggcctggag ataaaacttg tctcctctac caccacctg 120  
 taccctagcc tgcacctgtc ctcatctctg caaagtacag ctccctccc caggctctctg 180  
 tgccactctg tcttgatgc tctggggagc tcatgggttg aggagtctcc accagagggg 240  
 ggctcagggg actggttggg ccagggatga atatttgagg gataaaaatt gtgtaagagc 300  
 caaagaattg gtagtagggg gagaacagag aggagctggg ctatgggaaa tgatttgaat 360  
 aatggagctg ggaatatggc tgatatctg gtactaaaaa agggctctta agaacctact 420  
 tctaatactc ttcccacatg caaaccatag ctgtctgtcc agtgctctct tctgcctcc 480  
 agctctgccc caggctctc ctagactctg tccctgggct agggcagggg aggagggaga 540  
 gcagggttgg gggagaggct gagggagagtg tgacatgtgg ggagaggacc agacctgccc 600  
 gggcgccgct cg 612

<210> 57  
 <211> 363  
 <212> DNA  
 <213> Homo sapien

<400> 57  
 gtcgcggcgcg aggtccctgag cgtcacccta gttctgcccc ttttttagctg tgtagacttg 60  
 gacaagacat ttgacttccc tttctccttg tctataaaat gtggacagtg gacgtctgtc 120  
 acccaagaga gttgtgggag acaagatcac agctatgagc acctcgcacg gtgtccagga 180  
 tgcacagcac aatccatgat gcgtttttctc cccttacgca ctttgaaacc catgctagaa 240  
 aagtgaatac atctgactgt gctccactcc aacctccagc gtggatgtcc ctgtctgggc 300  
 cctttttctg ttttttattc tatgttcagc accactggca ccaaatacat ttttaattcac 360  
 cga 363

<210> 58  
 <211> 750  
 <212> DNA  
 <213> Homo sapien

<400> 58  
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 ctgcgcctct ctcccaactc gcgtgcctca cagaaccacg gtgctgcaca gccccgagat 120  
 gtggcccttc ttcaggaaaag agcaaataag ttggtccaag tacttgatgc ttaaggaata 180  
 cacaagggtg cccatcaagc gctcagaaat gctgagagat atcatccgtg aatacactga 240  
 tgttttatcca gaaatcattg aacgtgcatg ctttgtccta gagaagaaat ttgggattca 300  
 actgaaagaa attgacaaaag aagaacacct gtatattctc atcagtaccc ccgagtcctc 360  
 ggctggcata ctgggaacga ccaaagacac acccaagctc ggtctcttct tgggtattct 420  
 ggggtgtcatc ttcattgaatg gcaaccgtgc cagttaggct gtcttttggg aggcactacg 480  
 caagatggga ctgcgtcctg gggtagagaca tcccctccct tggagatcta aggaaacttc 540  
 tcacctatga gtttgtaaag cagaaatacc tggactacag acgagtgcgc aacagcaacc 600  
 ccccgagta tgagttcctc tggggcctcc gtccctacca tgagactagc aagatgaaaa 660  
 tgctgagatt cattgcagag gttcagaaaa gagaccctcg tgactggact gcacagttca 720  
 tggaggctgc agatgaggac ctgcccgggc 750

<210> 59  
 <211> 505  
 <212> DNA  
 <213> Homo sapien

<400> 59  
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 ttccagccgc agttctttta taagctttta gtgcctcatg aagacgcgag gatctcttcc 120  
 aagtgaacc ttggtcacatc agggcacatt cagcagcaga agtctgttcc cagtatagtc 180  
 cttggtatgg ctaaattcca ctgtcccttt ctccagcagtc aataatccat gataaattct 240  
 gtacaacact gtagtcaata acagcagcac cagacagcat attaatctt ttaccataaa 300  
 tttgtgtgta attataatgt tctatgtgtg gtgttatcaa aagaatcact gtgtctctaa 360  
 atatcatata tgtatgtctg gataaatata ttgctgtaca acatctccaa catgcaggtc 420  
 atgctctaag acttggggat atagagtaat acatgtttcg tggacctcg ccgcgaccac 480  
 gctaagggcg aattctgcag atatc 505

<210> 60  
 <211> 520  
 <212> DNA  
 <213> Homo sapien

<400> 60  
 cgtggtcgcg gccgaggtcc tcaggacaag gaaacaggta tcagcatgat ggtagcagaa 60

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accttatcac caaggtgcag gagctgactt cttccaaaga gttgtgggtc cgggcagcgg 120
tcattgcctg cccttgctgg agggctgatt ttagtggtgc ttattatgtt ggccctgagg 180
atgcttcgaa gtgaaaataa gaggctgcag gatcagcggc aacagatgct ctcccgtttg 240
cactacagct ttcacggaca ccattccaaa aaggggcagg ttgcaaagt agacttggaa 300
tgcatgggtc cggtcagtgg gcacgagaac tgctgtctga cctgtgataa aatgagacaa 360
gcagacctca gcaacgataa gatcctctcg cttgttcact ggggcatgta cagtgggcac 420
gggaagctgg aattcgtatg acggagtctt atctgaacta cacttactga acagcttgaa 480
ggacctgccc gggcgccgc tcgaaagggg cgaattctgc 520

```

<210> 61  
 <211> 447  
 <212> DNA  
 <213> Homo sapien

```

<400> 61
agagaggtgt ttttattctt tggggacaaa gccgggttct gtgggtgtag gattctccag 60
gttctccagg ctgtagggcc cagaggctta atcagaattt tcagacaaaa ctggaacctt 120
tcttttttcc cggttggttta ttgtagtcc ttgggcaaac caatgtcttt gttcgaaaga 180
gggaaaataa tccaaacgtt tttcttttaa cttttttttt aggttcaggg gcacatgtgt 240
aggcttgcta tataggtaaa ttgcatgtca ccagggtttg ttgtacagat tatttcatca 300
tccagataaa aagcatagta ccagataggt agttttttga tcttcaccct ctttccatgc 360
tccgacctca ggtaggcccc agtgtctgac ctgcccgccg gcccgctcga aagggccaat 420
tctgcagata tccatcacac tggccgg 447

```

<210> 62  
 <211> 83  
 <212> PRT  
 <213> Homo sapien

```

<400> 62
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
1          5          10          15
Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser Asp
20          25          30
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
35          40          45
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
50          55          60
Arg Asn Phe Pro Ile Pro Ile Pro Ser Ala Pro Thr Thr Pro Leu Pro
65          70          75          80
Ser Glu Lys

```

<210> 63  
 <211> 683  
 <212> DNA  
 <213> Homo sapien

```

<400> 63
acaaagattg gtagctttta tattttttta aaaatgctat actaagagaa aaaacaaaag 60
accacaacaa tattccaaat tatagggtga gagaatgtga ctatgaagaa agtattctaa 120
ccaactaaaa aaaatattga aaccactttt gattgaagca aaatgaataa tgctagattt 180
aaaaacagtg tgaatcaca ctttggtctg taaacatatt tagctttgct ttctattcag 240
atgtatacat aaacttattt aaaatgtcat ttaagtgaac cattccaagg cataataaaa 300
aaagwggtag caaatgaaaa ttaaagcatt tatttttgta gttcttcaat aatgatrcga 360
gaaactgaat tccatccagt agaagcatct ctttttgggt aatctgaaca agtrccaacc 420
cagatagcaa catccactaa tccagcacca attccttcac aaagtccttc cacagaagaa 480
gtgcgatgaa tattaattgt tgaattcatt tcagggtctc cttggtccaa ataaattata 540

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gcttcaatgg gaagaggtcc tgaacattca gctccattga atgtgaaata ccaacgctga 600  
 cagcatgcat ttctgcattt tagccgaagt gagccactga acaaaactct tagagcacta 660  
 tttgaacgca tctttgtaaa tgt 683

<210> 64  
 <211> 749  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> misc\_feature  
 <222> 534  
 <223> n = A,T,C or G

<400> 64  
 ctgttcattt gtccgccagc tcctggactg gatgtgtgaa aggcatacaca ttccattttt 60  
 cctccgtgta aatgttttat gtgttcgcct actgatccca ttcggtgctt ctattgtaaa 120  
 tatttgtcat ttgtatttat tatctctgtg ttttccccct aaggcataaa atgggtttact 180  
 gtgttcattt gaacccattt actgatctct gttgtatat ttccatgccca ctgctttgtt 240  
 ttctcctcag aagtcgggta gatagcattt ctatcccatc cctcacgtta ttggaagcat 300  
 gcaacagtat ttattgctca gggctctctg cttaaaactg aggaaggctc acattcctgc 360  
 aagcattgat tgagacattt gcacaatcta aaatgtaagc aaagtaagtc attaaaaata 420  
 caccctctac ttgggcttta tactgcatac aaatttactc atgagccttc ctttgaggaa 480  
 ggatgtggat ctccaaataa agatttagtg tttattttga gctctgcac ttanacaagat 540  
 gatctgaaca cctctccttt gtatcaataa atagccctgt tattctgaag tgagaggacc 600  
 aagtatagta aaatgctgac atctaaaact aaataaatag aaaacaccag gccagaacta 660  
 tagtcatact cacacaaagg gagaaattta aactcgaacc aagcaaaagg cttcacggaa 720  
 atagcatgga aaaacaatgc ttccagtgg 749

<210> 65  
 <211> 612  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 acagcagcag tagatggctg caacaacctt cctcctaccc cagcccagaa aatatttctg 60  
 cccaccccca ggatccggga ccaaaataaa gagcaagcag gcccccttca ctgaggtgct 120  
 gggtagggct cagtgccaca ttactgtgct ttgagaaaga ggaaggggat ttgtttggca 180  
 ctttaaaaat agaggagtaa gcaggactgg agaggccaga gaagatacca aaattggcag 240  
 ggagagacca ttggcgcca gtcccctagg agatgggagg agggagatag gtatgaggg 300  
 aggcgctaag aagagtagga ggggtccact ccaagtggca ggggtgctgaa atgggctagg 360  
 accaacagga cactgactct aggtttatga cctgtccata cccgttccac agcagctggg 420  
 tgggagaaat caccattttg tgactttctaa taaaataatg ggtctaggca acagttttca 480  
 atggatgcta aaacgattag gtgaaaagtt gatggagaat ttttaattcag gggaattagg 540  
 ctgataccat ctgaaacat ttggcatcat taaaaatgtg acaacctggt ggctgccagg 600  
 gaggaagggg ag 612

<210> 66  
 <211> 703  
 <212> DNA  
 <213> Homo sapiens

<400> 66  
 tagcgtggtc gcggccgagg tacattgatg ggctggagag cagggttggc agcctgttct 60  
 gcacagaacc aagaattaca gaaaaaagtc caggagctgg agaggcaca catctccttg 120  
 gtagctcagc tccgccagct gcagacgcta attgctcaaa cttccaacaa agctgccag 180  
 accagcaatt gtgttttgat tcttcttttt tccctggctc tcatcatcct gccagcttc 240  
 agtccattcc agagtgcacc agaagctggg tctgaggatt accagcctca cggagtgact 300

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tccagaaata tcctgaccca caaggacgta acagaaaatc tggagaccca agtggtagag 360
tccagactga gggagccacc tggagccaag gatgcaaatg gctcaacaag gacactgctt 420
gagaagatgg gagggagacc aagacccagt gggcgcatcc ggtccgtgct gcatgcagat 480
gagatgtgag ctggaacaga ccttcctggc ccacttctctg atcacaagga atcctgggct 540
tccttatggc ttgtcttccc actgggattc ctacttaggt gtctgccctc aggggtccaa 600
atcacttcag gacaccccaa gagatgtcct ttagtctctg cctgaggcct agtctgcatt 660
tgtttgcata tatgagaggg tacctgcccg ggcggccgct cga 703

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&lt;210&gt; 67

&lt;211&gt; 1022

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

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cttgagaaag caggattgtt ttaagttcca agatttaaca aacttactgt tcagcatcat 60
attcaagcct aaaaggaaga taggattttc aagatatatt tccaacttct ttaacatggc 120
accatggatg aactgtttct cagcactgtg ctgcttcaact tgggaattaag gatgaattgg 180
gaggagacag tatgacatag gtgggttaggt tgggtggtga ggggaaccag ttctaatagt 240
cctcaactcc actccagctg ttctctgtcc acacgggtcca ctgagctggc ccagtccctt 300
tcactcagtg tgtcaccaaa ggcagottca aggtcfaatg gcaagagacc acctataacc 360
tcttcacctt ctgctgcctc ttctctgtgc cactgactgc catggccatc tgctatagcc 420
gcattgtcct cagtgtgtcc agggcccaga caagggaagg gagccatggg gagactccaa 480
ttccagggcc ttaatcctta accctagacc tgttgccctc agcatcattt atttatctac 540
ctacctaata gctatctacc agtcattaaa ccatggtgag attctaacca tgtctagcac 600
ctgatgctag agataatttt gttgaatccc ttcaattata aacagctgag ttagctggac 660
aaggactagg gaggcaatca gtattattta ttcttgaaca ccatcaagtc tagacttggg 720
ggcttcatat ttctatcata atccctgggg gtaagaaaatc atatagcccc aggttgggaa 780
ggggaaaacg gtttgcaaca ttctcctcct tgtaggaggc gagctctgtc tcactagcta 840
tgcccctcca tcaattcacc ctatactcag atcagaagct gagtgtctga attacagtat 900
atthttctaaa ttctagccc ctgctgggtga atttgccctc ccccgctcct ttgacaattg 960
tcccctgtgt cgtctccggg ccctgagact ggccctgctt atcttgtctga ccttcatcct 1020
ct 1022

```

&lt;210&gt; 68

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

```

ccagatccat ttccagtggg ctggatttct ttttattttc ttttcaactt gaaagaaact 60
ggacattagg ccactatgtg ttgttactgc cactagtgtt caagtgcctc ttgttttccc 120
agagatttcc tgggtctgcc agaggcccag acaggctcac tcaagctctt taactgaaaa 180
gcaacaagcc actccaggac aaggttcaaa atgggttaca cagcctctac ctgtcgcccc 240
agggagaaaag gggtagtgat acaagtcca tagccagaga tgggtttcca ctccttctag 300
atattcccaa aaagaggctg agacaggagg ttattttcaa ttttattttg gaattaaata 360
cttttttccc ttattactg ttgtagtccc tcacttggat atacctctgt tttcacgata 420
gaaataaggg aggtctagag cttctattc 449

```

&lt;210&gt; 69

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

<222> 22, 26, 36, 45, 54, 56, 62, 63, 73, 92, 98, 105, 155, 174,  
194, 302, 312, 358, 375, 378, 381

&lt;223&gt; n = A,T,C or G

<400> 69  
 gcccttagcg tgggtcgagg cncgangtct ggagcntatg tgatncctat ggtncncagg 60  
 cnnatactgc tantctcatt tattctcctg cnacctantc ctctnctctg gaatcacacc 120  
 attattgcct gttaacactg gactgtgagt accangcaat taatttgac caanaaagt 180  
 gaggggtatta tcanatattg caatctgtac agaggggaaga tgatttcaat ttgatttcaa 240  
 cttaaccttc atctttgtct gttaacacta atagaggggtg tctaataaaa tggcaaattt 300  
 gngatctcat tnggtataac tacactcttt ttcacagatg tgatgactga atttccanca 360  
 acctgcccgg gcgngcngtc naagggc 387

<210> 70  
 <211> 836 -  
 <212> DNA  
 <213> Homo sapiens

<400> 70  
 tattccattt aaaaaataaa ttcagccctg cactttcttt agatgccttg atttccagaa 60  
 tggagcttag tgctactgaa taccctggcc acagagccac ctcaggatat tcttttctcc 120  
 accctagttt atttatttat agatatctgt ttacaaagtc tgtagtaaat cctgatgctg 180  
 accatctgaa atgtactttt tttctgaatg ctgtttcaat ctaaaatagc agcttttgag 240  
 aaaaacaatga tgtaaattcc ttatgataaa aggatgattc tatatatctt ttaatgatat 300  
 taaatatgcc gaagccaagc acacagtctt tctaaagtgt gtgtatgttt gtgtgaatgt 360  
 gaatgatact gatcttataat ctgttaaaag ttgttttaaa aagctgtggc atccatttgt 420  
 tcataatttc caagtcttct gtaaagatgt ctaggacgaa atattttatg tgctaatagca 480  
 tgtatttgta aaccagattt gtttaccact caaaaataac ttgttttctt catccaaaaa 540  
 agtttatttc ttccacgtac tttaaatttc tgtgtgggta taatatagct ttctaatttt 600  
 tttctttcac aaaggcaggt tcaaaattct gttgaaagaa aaatgcttcc tgaactgag 660  
 gtataacacc agagcttgct gtttaaagga ttatatgatg tacatcagtt ctataaatgt 720  
 gctcagcagt ttaacatgtg aatcctgttt taaagtgtct agatttcaac tgtgtaagcc 780  
 attgatataa cgctgtaatt aaaaatgttt atatgaaaaa aaaaaaaaaa aaaaaa 836

<210> 71  
 <211> 618  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 tccacaggag caatttggtt accttttttt tctgatgctt tactaacttc atctttttaga 120  
 tttaaatcat tagtagatcc tagaggagcc agtttcagaa aatatagatt ctagtccagc 180  
 accaccgcta gttgtgcatt gaaataatta tcattatgat tatgtatcag agcttctggg 240  
 tttctcattc tttattcatt tattcaacaa ccacgtgaca aacactggaa ttacaggatg 300  
 aagatgagat aatccgctcc ttggcagtggt tatactatta tataacctga aaaaacaaac 360  
 aggttaattt cacacaaagt aatagatatc atgacacatt taaaataggg cactactgga 420  
 acacacagat aggacatcca ggttttggtt caatattgta gacttttttg tggatgagat 480  
 atgcagggtg atrccagaag gacaacaaaa acatatgtca gatagaaggg aggagcaa 540  
 gccaaagagct ggagctgagg aagatcactg tgaatttcta tgtagtctag ttggctggat 600  
 gctagagcaa agaggtgg 618

<210> 72  
 <211> 806  
 <212> DNA  
 <213> Homo sapiens

<400> 72  
 tctacgatgg ccatttgctc attgtctttc ctctgtgtgt agtgagtga cctggcagtg 60  
 tttgcctgct cagagtggcc cctcagaaca acagggtgg ccttggaana accccaaaac 120  
 aggactgtgg tgacaactct ggtcagggtg gatttgacat gagggccgga ggcggttgct 180

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gacggcagga ctggagagggc tgcgtgcccg gcactggcag cgaggctcgt gtgtccccc 240
ggcagatctg ggcactttcc caaccagggt ttatgccgtc tccagggaag cctcgggtgcc 300
agagtgggtg gcagatctga ccatccccc acaccagaaa caaggaattt ctgggattac 360
ccagtccccc ttcaaccag ttgatgtaac cacctcattt ttacaaata cagaatctat 420
tctactcagg ctatgggcct cgtcctcact cagttattgc gagtgttgct gtccgcattgc 480
tccgggcccc acgtgggtcc tgtgtctag atcatggtga cccccgcc ctgtggttg 540
aatcgatgcc acggattgca ggccaaattt cagatcgtgt ttccaaacac ccttgctgtg 600
ccctttaatg ggattgaaag cacttttacc acatggagaa atatattttt aatttgtgat 660
gcttttctac aagggtccact atttctgagt ttaatgtgtt tccaacactt aaggagactc 720
taatgaaagc tgatgaattt tcttttctgt ccaaacaagt aaaataaaaa taaaagtcta 780
tttagatggt gaaaaaaaa aaaaaa 806

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<210> 73
<211> 301
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 59
<223> n = A,T,C or G

```

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<400> 73
actctggtta gcttgttgtt gtccaagtga agctccctca gatgaggcgt gttggccana 60
gagccattgt caacagcaga gatgctgttg aaactcaatc ccaacttagc caaattattc 120
agtcctttca ggctagctgc atcaactctg ctgattttgt tgccatcaag atgtaattcc 180
gtaagggaa gaggagacc ttgaggaatg ctggygatat tggycatcagc aatgcggatg 240
tasgaagagc ttcttcmctc cctggaaagc cccattttca atyccttgag ctcttcakcg 300
g 301

```

```

<210> 74
<211> 401
<212> DNA
<213> Homo sapiens

```

```

<400> 74
agtttcatg atccctgtaa cagccatggt ctcaaactca gatgcttcct ccatctgcca 60
agtgtgttct ggatacagag cacatcgtgg cttctgggg cactcagc ttaggctgtg 120
gggtccacaga gcactcatct ggctgggcta tgggtgggtt ggctctactc aagaagcaaa 180
gcagttacca gcacattcaa acagtgtatt gaacatcttt taaatatcaa agtgagaaac 240
aagaaggcaa cataataatg ttatcagaaa gatgttagga agtaaggaca gctgtgtaaa 300
gcttgaggct gaaaagtagc ttgccagctt catttctttg gtttcttggg tagtgggccg 360
ccggaacagc aagatgtgag gttctggttc atggatcata t 401

```

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<210> 75
<211> 612
<212> DNA
<213> Homo sapiens

```

```

<400> 75
ttatttttca atttttattt tggttttctt acaaagggtg acattttcca taacaggtgt 60
aagagtgttg aaaaaaaaa tcaaattttt ggggagcgag ggaaggagtt aatgaaactg 120
tattgcacaa tgctctgatc aatccttctt tttctctttt gccacaaatt taagcaagta 180
gatgtgcaga agaaatggaa ggattcagct ttcagttaaa aaagaagaag aagaaatggc 240
aaagagaaag ttttttcaaa tttcttctt ttttaattta gattgagttc atttatttga 300
aacagactgg gccaatgtcc acaaagaatt cctggtcagc accaccgatg tccaaagggtg 360
caatatcaag gaagggcagg cgtgatggct tatttgtttt gtattcaatg attgtcttct 420
ccattcatt tgtcttttta gagcagccat ctacaagaac agtgaagtg aacctgctgt 480

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```

tgccctcagc aacaagttca acatcattag agccctgtag aatgacagcc tttttcaggt 540
tgccagtctc ctcatocatg tatgcaatgc tgttcttgca gtggtaggtg atgttctgag 600
aggcatagtt gg                                     612

```

```

<210> 76
<211> 844
<212> DNA
<213> Homo sapiens

```

```

<400> 76
ggcttttcgag cggccgcccg ggcaggtctg atggttctcg taaaaacccc gctagaaact 60
gcagagacct gaaattctgc catcctgaac tcaagagtgg agaatactgg gttgacctta 120
accaaggatg caaattggat gctatcaagg tattctgtaa tatggaaact ggggaaacat 180
gcataagtgc caatcctttg aatgttccac ggaacacctg gtggacagat tctagtgtctg 240
agaagaaaca cgtttggttt ggagagtcca tggatgggtg ttttcagttt agctacggca 300
atcctgaact tcctgaagat gtcttgatg tgcagcykgc attccttoga cttctctcca 360
gccgagcttc ccagaacatc acatatcact gcaaaaatag cattgcatac atggatcagg 420
ccagtggaaa tgtaagaag gccctgaagc tgatggggtc aaatgaaggc gaattcaagg 480
ctgaaggaaa tagcaaattc acctacacag ttctggagga tggttgcacg aaacacactg 540
gggaatggag caaaacagtc tttgaatatc gaacacgcaa tgctgttctt tgacattgca 600
ccaccaatgt ccagaggtgc aatgtcaagg aacggcaggc gagatggctt atttgttttg 660
tattcaatga ttgtcttgcc ccattcattt gtcttttttg agcagccatc gactaggaca 720
gagtaggtga acctgctgtt gccctcagca acaagttcca catcgttggg acctgcaga 780
agcacagcct tgttcaarct gcccgctctc tcatccagat acctcgcccg cgaccacgct 840
aatc                                     844

```

```

<210> 77
<211> 314
<212> DNA
<213> Homo sapiens

```

```

<400> 77
ccagtcctcc acttggcctg atgagagtgg ggagtggcaa gggacgtttc tcctgcaata 60
gacacttaga tttctctctt gtgggaagaa accacctgtc catccactga ctcttctaca 120
ttgatgtgga aattgctgct gctaccacca cctcctgaag aggcctccct gatgccaatg 180
ccagccatcc tggcatcctg gccctcagac aggcctgcggg aagtagcgat ctctgctcc 240
agccgtgtct ttatgtcaag cagcatcttg tactcctggt tctgagcctc catctcgcat 300
cggagctcac tcag                                     314

```

```

<210> 78
<211> 548
<212> DNA
<213> Homo sapiens

```

```

<400> 78
accaagagcc aagtgttaca caggatattt taaaaataaa atgttttttg aatcctcacc 60
tcccatgcta tcttctaaga taactacaaa tattcttcaa agatttaact gatttctgcc 120
aaggacctcc caggactcta tccagaatga ttattgtaaa gctttacaaa tcccaccttg 180
gccctagcga taattaggaa atcacaggca aacctcctct ctcgagagacc aatgaccagg 240
ccaatcagtc tgcacattgg ttttgttaga tactttgtgg agaaaaacaa aggctcgtga 300
tagtgcagct ctgtgcctac agagagcctc ccttttggtt ctgaaattgc tgatgtgaca 360
gagacaaaagc tgctatgggt ctaaaacctt caataaagta actaatgaca ctcaagggtc 420
tgggactctg agacagacgg tggtaaaacc cacagctgcg attcacattt ccaatttatt 480
ttgagctctt tctgaagctg ttgcttccta cctgagaatt cccatttaga gagctgcaca 540
gcacagtc                                     548

```

```

<210> 79
<211> 646

```

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

```
accccgtcac tatgtgaata aaggcagcta gaaaatggac tcaattctgc aagccttcat 60
ggcaacagcc catattaaga cttctagaac aagttaaaaa aaatcttcca ttcccatcca 120
tgcatgggaa aagggcttta gtatagttta ggatggatgt gtgtataata ataaaatgat 180
aagatatgca tagtggggga ataaagcctc agagtccttc cagtatgggg aatccattgt 240
atcttagaac cgagggattt gtttagattg ttgatctact aatttttttc ttcacttata 300
tttgaatttt caatgatagg acttattgga aattggggat aattctgttg tggattataa 360
taatattcat tttttaaaaa ctcatcttgg tattgagtta gtgcattgac ttccaatgaa 420
ttgacataag cccatatttc attttaacca gaaacaaaaa ctagaaaatg ttactcccta 480
aataggcaac aatgtatttt ataagcactg cagagattta gtaaaaaaca tgtatagtta 540
ctttagaaac aacttctgac acttgagggt tacccaatgg tctccttccc attctttata 600
tgaggtaaat gcaaaccagg gagccaccga ataaacagcc ctgagt 646
```

&lt;210&gt; 80

&lt;211&gt; 276

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

<222> 16, 29, 32, 45, 53, 55, 58, 59, 65, 66, 75, 77, 85, 90, 97,  
109, 112, 163, 170

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 80

```
gtctgaatga gcttcnctgc gagatgganc ancataaccc agaantccaa aancntanng 60
aacgnnaaaa cccgntngaa caagnaaacn gcaactnacg gccgcctgnt gnagggcgag 120
gacgccacc tctcctctc ccagttctcc tctggatgc agncatccan agatgtgacc 180
tcttcagcc gccaaatccg caccaaggtc atggatgtgc acgatggcaa ggtgggtgtc 240
cacccacgaa caggtccttc gcaccaagaa ctgagg 276
```

&lt;210&gt; 81

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 81

```
gtcctgcctt tcatcttttc ttttaaaaaa ataatgttt aaaaaacatt tccctcagat 60
tttaaaattc atggaagtaa taaacagtaa taaaatatgg atactatgaa aactgacaca 120
cagaaaaaca taaccataaa atattgttcc aggatacaga tattaattaa gagtgacttc 180
gttagcaaca cgtagacatt catacatatc cggtggaaga ctggtttctg agatgcgatt 240
gccatccaaa cgcaaatgct tgatcttggg taggrtaat ggcccagga tcttgacaga 300
gctctttatg tcaaacttct caagttgatt gacctcagg taatagtttt caaggttttc 360
attgacagtt ggtatgtttt taagcttgtt ataggacaga tccagctcaa ccagggatga 420
cacattgaaa gaatttcag gtattccact atcagccagt tcgttgtag ataaacgcag 480
atactgcaat gcattaaaac gcttgaaata ctcatcaggg atgttgctga tcttattgtt 540
gtctaagtag agagttagaa gagagacagg gagaccagaa ggcagtctgg ctatctgatt 600
gaagctcaag tcaaggtatt cgagtgtttt aagaccttta aaagcag 647
```

&lt;210&gt; 82

&lt;211&gt; 878

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 82

```

ccttctttcc ccactcaatt cttcctgccc tgttattaat taagatatct tcagottgta 60
gtcagacaca atcagaatya cagaaaaatc ctgcctaagg caaagaaata taagacaaga 120
ctatgatatc aatgaatgtg gggttaagtaa tagatttcca gctaaattgg tctaaaaaag 180
aatattaagt gtggacagac ctatttcaaa ggagcttaat tgatctcact tgttttagtt 240
ctgatccagg gagatcacc cttctaattat ttctgaactt gggttaataaa agttttataag 300
atttttatga agcagccact gtatgatatt ttaagcaaat atgttattta aaatattgat 360
ccttcccttg gaccaccttc atgttagttg ggtattataa ataagagata caacctatgaa 420
tatattatgt ttatacaaaa tcaatctgaa cacaattcat aaagatttct cttttataacc 480
ttcctcactg gcccctcca cctgcccata gtcaccaa tctgttttaa atcaatgacc 540
taagatcaac aatgaagtat ttataaatg tttttatgct gctagactgt ggggtcaaag 600
tttccatttt caaattattt agaattctta tgagttttaa atttgtaaat ttctaaatcc 660
aatcatgtaa aatgaaactg ttgctccatt ggagtagtct cccacctaaa tatcaagatg 720
gctatatgct aaaaagagaa aatatgggtc agtctaaaaa ggctaattgt cctatgatgc 780
tattatcata gactaatgac atttatcttc aaaacaccaa attgtcttta gaaaaattaa 840
tgtgattaca ggtagagaac ctcggccgcg accacgct 878

```

<210> 83  
 <211> 645  
 <212> DNA  
 <213> Homo sapiens

```

<400> 83
acaaacattt tacaaaaaag aacattacca atatcagtg cagtaagggc aagctgaaga 60
ataaatagac tgagtttccg ggcaatgtct gtcctcaaag acatocaaac tgcgttcagg 120
cagctgaaac aggttctttt cccagtgcac agcatatgtg gtcagtaata caaacgatgg 180
taaattgaggc tactacatag gccaggttaa caaactcctc ttctcctcgg gtaggcatg 240
atacaagtgg aactcatcaa ataattttaa cccaaggcga taacaacgct atttccatc 300
taaaactcatt taagccttca caatgtcgca atggattcag ttacttgcaa acgatcccg 360
gttgtcatac agatacttgt ttttacacat aacgctgtgc catcccttcc ttactgccc 420
cagtcagggtt tcctgttgtt ggaccgaaag gggatacatt ttgaaatgc ttccctcaag 480
acagaagtga gaaagaaagg agaccctgag gccaggatct attaaacctg gtgtgtgcgc 540
aaaagggagg gggaaggcag gaatttgaaa ggataaacgt ctcttttgcg ccgaggaaac 600
aggaagcgtg actcacttgg gtctgggacg ataccgaaat ccggt 645

```

<210> 84  
 <211> 301  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 270, 284  
 <223> n = A,T,C or G

```

<400> 84
tctgatgtca atcacaactt gaaggatgcc aatgatgtac caatccaatg tgaaatctct 60
cctcttatct cctatgctgg agaaggatta gaaggttatg tggcagataa agaattccat 120
gcacctctaa tcatcgatga gaatggagtt catgggctgg tgaaaaatgg tatttgaacc 180
agataccaag ttttgtttgc cacgatagga atagctttta tttttgatag accaactgtg 240
aacctacaag acgtcttgga caactgaagn ttaaataatcc acangggttt attttgcttg 300
g 301

```

<210> 85  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> misc\_feature  
<222> 16, 20, 240  
<223> n = A,T,C or G

<400> 85  
agcgtgggtc gcggcncgan gtagagaacc gactgaaacg tttgagatga agaaagtctt 60  
cctcctgatt acagccatct tggcagtggtc tgttggtttc ccagtctctc aagaccagga 120  
acgagaaaaa agaagtatca gtgacagcga tgaattagct tcagggtttt ttgtgttccc 180  
ttacccatatt ccatttcgcc cacttccacc aattccattt ccaagatttc catggtttan 240  
acgtaatttt cctattccaa tacctgaate tgcccctaca actccccttc ctagec 296

<210> 86  
<211> 806  
<212> DNA  
<213> Homo sapiens

<400> 86  
tctacgatgg ccatttgctc attgtctttc ctctgtgtgt agtgagtgc cctggcagtg 60  
tttgcttgct cagagtggtc cctcagaaca acagggtgtg ccttggaaaa accccaaaac 120  
aggactgttg tgacaactct ggtcaggtgt gatttgacat gagggccgga ggcggttgct 180  
gacggcagga ctggagaggt tgcgtgcccg gcactggcag cgaggctcgt gtgtccccc 240  
ggcagatctg ggcactttcc caaccaggt ttatgccgtc tccagggaag cctcggtgcc 300  
agagtgggtg gcagatctga ccattcccac agaccagaaa caaggaattt ctgggattac 360  
ccagtccccc ttcaaccag ttgatgtaac cacctcattt ttacaaaata cagaatctat 420  
tctactcagg ctatgggcct cgtcctcact cagttattgc gagtgttgct gtccgcatgc 480  
tccgggcccc acgtgggtcc tgtgctctag atcatggtga ctccccgcc ctgtggttg 540  
aatcgatgcc acggattgca ggccaaattt cagatcgtgt ttccaaacac ccttgctgtg 600  
ccctttaatg ggattgaaag cacttttacc acatggagaa atatattttt aatttgatg 660  
gcttttctac aagggtccact atttctgagt ttaatgtgtt tccaacactt aaggagactc 720  
taatgaaagc tgatgaattt tcttttctgt ccaacaagt aaaataaaaa taaaagtcta 780  
tttagatgtt gaaaaaaaa aaaaaa 806

<210> 87  
<211> 620  
<212> DNA  
<213> Homo sapiens

<400> 87  
tttttgcatt agatctgaaa tgtctgagag taatagtctt tgttgaattt tttttgttc 60  
atttttctgc acagtcatt ctgtttttat tactatctag gcttgaaata tatagtgtga 120  
aattatgaca tccttcctct ttgttatttt cctcatgatt gctttggcta ttcaaagttt 180  
attttagttt catgtaaat tttgaattgt attttccatt atttgaaaa tagtaccact 240  
gcaattttta taggaagttt attgaatcta tagattactt tggataatat ggcacttcaa 300  
taatattcat gttttcaatt catagacaaa atattttaaa atttatttgt atcttttcta 360  
atttttcctt tttttattgt aaagatttac ctcccttggt aatattttcc tcagaaattt 420  
attatttaag gtatagtcaa taaaattttc ttcctctatt ttgtcagata gtttaagtgt 480  
atgaaacat agatatactt gtatgttaat tttatatttt gctaatttac tgagtgtatt 540  
tattagttaa gagaggtttt aatgtactgt ttatggtttt ttaaataata gattacttat 600  
tttttaaaaa aaaaaaaaaa 620

<210> 88  
<211> 308  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 9, 189, 194, 206, 238, 296

<223> n = A,T,C or G

<400> 88

```
tagctgtgnt cagcaggccg aggttttttt tttttttgag atggagtctc gccctgtcac 60
ccaggctgga gtgcagtgga ctgatctcag ctcaactgaa gctccacctc ctggattcac 120
gctattctcc tgccctcagcc tcccaagtag ctgggactac aggcgcccgc caccacgccc 180
agctaattnt ttgnattttt agtacnagat gcggtttcat cgtgttagcc agcatgggct 240
cgatctcctg acctcgtgaa ctgcccgcct cggcctccca aagacctgcc cgggcnggcc 300
gctcgaaa                                     308
```

<210> 89

<211> 492

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 448

<223> n = A,T,C or G

<400> 89

```
agcggccgcc cgggcaggtc tgttaagtaa catacatatc accttaataa aaatcaagat 60
gaaatgtttt agaaactatt ttatcaaaag tggtcttgat acaaagactt gtacatgatt 120
gttcacagca gcactattaa tgccaaaaag tagacaaaac cttaatgtcc attaatgat 180
aagcaaaatg tggatatatc atacaatgga atattatgta gcccaaca tgatcatgag 240
tactacaaca tggatgagcc tcaaaaacgt tatgctaaat gaaaaaagtc agatatagga 300
aaccacatgt catatgatcc cttttatatg aaatagccag aaaaggcaag tcatagaaac 360
aagatagatc ggaaaatggg ttggaggact acaaattgca ccagggatct ttgaagtga 420
tggaatgggt ctaaaatcag actgtggnag tggttgaaca agtctgtaaa ttaccacaaa 480
tgcgttaata ca                                     492
```

<210> 90

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 106, 184, 206, 209, 234, 314

<223> n = A,T,C or G

<400> 90

```
tcgagcggcc gcccgggcag gtacaagctt tttttttttt tttttttttt ttttctaaca 60
gttctctgtt ttattgcaat acagcaaagt ctggttaata ttaagngata tcaacataaa 120
gtattgtgga ggagtctttt gtgacatttt ttaccatccc accttaataa tttctgtgca 180
aaanaatcca catcattggt tggatcancg ggatctctta aaaagttccc taanacactg 240
agggcataaa accaaacaaa ataaaataag gagtgatagg ctaaagcagt atcttcccct 300
ccatccacat ttgncaagca ttatattcta accaaaaaat gatcacacca ggccatgcaa 360
aactgtccaa tattaccgag aaaaaaccct                                     390
```

<210> 91

<211> 192

<212> DNA

<213> Homo sapiens

<400> 91

```
agcgtggtcg cggccgaggt ctgtcaatta atgctagtcc tcaggattta aaaaataatc 60
ttaactcaaa gtccaatgca aaaacattaa gttgtaatt actcttgatc ttgaattact 120
```

tccggttacga aagtccttca cttttttcaa actaagctac tatatttaag gcctgcccgg 180  
gcggccgctc ga 192

<210> 92  
<211> 570  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 519, 559  
<223> n = A,T,C or G

<400> 92  
agcgtggctcg cggccgaggt ctgacaacta acaaagaagc aaaaactggc atcttggaca 60  
tcctagtatt acacttgcaa gcaattagaa cacaaggagg gccaaggaaa aagtttagct 120  
ttgaatcact tccaaatcta ctgattttga gggtccgcag tagttctaac aaaacttttc 180  
agacaatggt aactttcgat taagaaagaa aaaaacccca aacatcttca ggaattccat 240  
gccagggttca gtctcttoca gtgagcccgcc ttgctaaaag tccacgtgca ccattaatta 300  
gctgggcttg cagcaccatg taaaaagaag cctattcacc accaaccaca cagactagac 360  
atgtaaagta ggatcaagta atggatgaca accatggctcg tggaatatgg tcaatgagag 420  
tcagaaaagt acaggcacca gtacaagcag cagataacag aattgacggg ccaaaggata 480  
aaaataggct tatttaaata ggatgctaca gaacacatnc acttctaatt ggaagctgct 540  
ttacactggg tggcattgna ccatatgcat 570

<210> 93  
<211> 446  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 328, 389  
<223> n = A,T,C or G

<400> 93  
tcgagcggcc gcccgggcag gtccagggtt ttatttagtt gtgtaatctt ggacaagtta 60  
cctaactttt ttgagtctga atatatttaa tctgcaaaat gagaatcatg ataatacgtc 120  
ataggcttaa ttagggagat taaatgaaat aatttatagg tggtgccatg gttacatata 180  
agtattagta gtaattctt ttcccttggt tacttttata gtatagggtg gatgaagggt 240  
ccagtatagg caaaaatact acttgggggt aaagtagagt gtgatacttt atttgaaatg 300  
ttccctgaat ctgatcttta ctttttgnta ctgctgcact acccaaattc aaattttcat 360  
cccaacattc ttggatttgt gggacagcng tagcagcttt tccaatataa tctatactac 420  
atcttttctt actttggtgc tttttg 446

<210> 94  
<211> 409  
<212> DNA  
<213> Homo sapiens

<400> 94  
cgagcggccg cccgggcagg tccatcagct cttctgctta gaatacgagg cagacagtgg 60  
agaggtcaca tcagttatcg tctatcaggg tgatgaccca agaaagggtga gtgagaagggt 120  
gtcggcacac acgcctcttg atccaccat gcgagaagcc ctcaagttgc gtatccagga 180  
ggagattgca aagcgcagga gccaacactg accatggtga aggcgttctc tccaggctgg 240  
attcactgca ctcggaagaa ttctgcccag ggaatttagt gtgggggtac caggaccagt 300  
ttgtcttgat cttgagaccc ccagagctgc tgcattccata ggggtgtgca ggactacacc 360  
tggcctgcct tgcagtcatt ctttcttata tgttgaccca tttgcccga 409

<210> 95  
<211> 490  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 486  
<223> n = A,T,C or G

<400> 95  
tcgagcggcc gcccgggcag gtccacttg tttgcagctt ccacacactg cacctaccta 60  
ctacctctct tccatgctta actgggttta gaaaggtgag ctatgcgtag aagaactact 120  
tgggatattc aagtgcgtga tttgaacgat aagcctatag ataacagtct gaagctgcaa 180  
gggagacttt gttagtacac tactataaac aggtaaacta cctgtttgta cttgatatag 240  
tgcatatgaa atgactgatt taatacaaaa ctacagaaca tgcaaaattt tttctgagat 300  
gttaagtatt acttcagtgg agaacaaaac ttacttaacc tttcgtaat gcatgtagta 360  
ccagaaagca aacatgggtt tagcttcctt tactcaaaat atgaacatta agtggttgtg 420  
aattttgtct gccaaagtgt tcagaaaata cattataaat aacctaagtt aaaaaaaga 480  
aactgngaac 490

<210> 96  
<211> 223  
<212> DNA  
<213> Homo sapiens

<400> 96  
agcgtgggtc cggccgaggt ctggaagccc accctaggac ttgaatggca ccttgcctt 60  
tctctgccag taatgcaatc caacacaata tgctacaggg aaaacagaat ttccacggtg 120  
ccgccctctg gtacaaggga aacagcacgc aaagcaaaag gccacagagg gctccctgag 180  
aatccagtac aactaagcga ggacctgccc gggcgccgc tcg 223

<210> 97  
<211> 527  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 404, 436, 451, 476  
<223> n = A,T,C or G

<400> 97  
tcgagcggcc gcccgggcag gtctgtgcag gagacactga agtgggtagt gtccataatc 60  
tttttagcct gttgctgaaa ttccagttgt actccttcaa accaaaatgc ttacaggatc 120  
atgggaaagc ctcggttgca gaaatcaaga caggcaagtg ggaagataac tcggccttga 180  
gggttaaacag atctgggttc aaagcatagt ttactctct gtcttgtaga gtgtcctggg 240  
tgaagtcatt tcctctcttg aatttcagag aggatgaaaa tataaaaagt ataataacta 300  
tcttcataat ctttgtgagg attaaagaag acgaagtgtg tgaaaagcta agcacagagc 360  
aggcattcta caataagtag ttattatttt tggaaccatc ccgnccctag cccagccca 420  
attaccttct cttagnctct tcatatcgaa ngccgtaatc ttgacottct cttgcnactg 480  
gattggtgct ggttgatgcc caaacttccc gagatgctgt ctgggaa 527

<210> 98  
<211> 514  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 455

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 98

```
tcgagcggcc gcccgggcag gtctggctcc catggccctt ggggtggcct gactctgtca 60
ctattcctaa aaccttctag gacatctgct ccaggaagaa ctttcaacac caaaattcat 120
ctcaatttta cagatgggaa aagtgattct gagaccagac cagggtcagg ccaagggtcat 180
ccagcatcag tggctgggct gagactgggc ccaggaacc ctgtctgtct ctctttttcc 240
cagagctgtg agttctctag ccaaggctgc actcttgagg gagagccagg aagcatagct 300
gaggccatga caacctcact cttcacctga aaatttaacc cgtggcagag gatccaggca 360
catataggct tcggagccaa acaggacctc ggccgcgacc acgctaagcc gaattccagc 420
aactggcgg ccgttactag tggatcccg gcttnggtac caagcttggc gtaatcatgg 480
gcatagctgg ttcctggggg gaaaatggta tccg 514
```

&lt;210&gt; 99

&lt;211&gt; 530

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 430, 522

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 99

```
tcgagcggcc gcccgggcag gtctgaagaa acaggataaa atttggcagc cagtaatttt 60
gacaggggaag ttacagcttg catgacttta aatatgtaaa ttgaaaata ctgaatttcg 120
agtaatcatt gtgctttgtg ttgatctgaa aaatataaca ctggctgtcg aagaagcatg 180
ttcaaaaata tttaatccac ttcaaaatgt catataaatt atgggtggtt ctatgcaccc 240
ctaaagcttc aagtcattta gctcaggtag atactaaagt aatatattaa ttcttccagt 300
acagtgggtg ttcataccat tgacatttgc ataccctaga ataatttaag aaagacatgt 360
gtaaatattca caatgttcag aaaagcaagc aaaagggtcaa ggaacctgct ttggttcttc 420
tgagatggn ctcataatcag cttcataaac attcattcta caaaatagta agctaaccat 480
ttgaaccca atttcagat taagcatatt ttctcataaa tnatgaagcc 530
```

&lt;210&gt; 100

&lt;211&gt; 529

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 100

```
agcgtggctg cggccgaggt ccaggcacgg tggcttatgt gtgtaatccc agcacttggg 60
gaggctgagg gaggtggatc acttgagtc aggagtttga gaccagtctg ggcaacatgg 120
cgaaacttca tcaactaccaa agaagaaaaa aattagccag gtgtggtggt gtatgcctgt 180
agtccagat actctggtgg ctgaggtgag aggatagctt gagcccagga aattgaggct 240
gcagtgaact atgattgcac tactgtgctc cagcttgggc aacagagtga gatcttgtct 300
ccaaaagtcc ttgaaggatt ttaggaagtt gttaaaagtc ttgaaacgat gtttgggggc 360
atgttagggt tcttgaatgt ttaattcctc taataactgc ttattcaaga gaagcatttc 420
tgactgggtg cggggcagtg gcttcatgcc ccataatccc agtactttgg gaggctgaag 480
caggaacatt gcttgagccc aggacttcaa gaacagcctg ggtaacata 529
```

&lt;210&gt; 101

&lt;211&gt; 277

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

```

tcgagcggcc gcccgggcag gtcgcaggaa gaggatggaa actgaggagt ccaggaagaa 60
gagggaaacga gatccttgagc tggaaatggg agatgattat attttggatc ttcagaagta 120
ctgggatttta atgaatttgt ctgaaaaaca tgataagata ccagaaatct gggaaggcca 180
taatatagct gattatattg atccagccat catgaagaaa ttggaagaat tagaaaaaga 240
agaagagctg agaacagacc tcggccgcga ccacgct 277

```

&lt;210&gt; 102

&lt;211&gt; 490

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

```

gcgtggtcgc ggccgaggtc tgacggcttt gctgtcccag agccgcctaa acgcaagaaa 60
agtcgatggg acagttagag gggatgtgct aaagcgtgaa atcagttgtc ctttaattttt 120
agaaagattt tggtaactag gtgtctcagg gctgggttgg ggtccaaagt gtaaggaccc 180
cctgccctta gtggagagct ggagcttggg gacattacc cttcatcaga aggaattttc 240
ggatgttttc ttgggaagct gttttgggtcc ttggaagcag tgagagctgg gaagcttctt 300
ttggtctctag gtgagttgtc atgtgggtaa gttgaggtta tcttgggata aagggtcttc 360
tagggcacaa aactcactct aggtttatat tgtatgtagc ttatatattt tactaagggtg 420
tcaccttata agcatctata aattgacttc tttttcttag ttgtatgacc tgccccgggc 480
ggccgctcga 490

```

&lt;210&gt; 103

&lt;211&gt; 490

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 103

```

gagcggccgc ccgggcaggc ccaaaccagc ttgtctataa gtcattaacc aaatccatta 60
taggtaattt gttcagttca atgtttacaa ttcttatgga aaaaattagc aacacacaca 120
tttaaaacgt gtgcatttac ctttgcgtga gtgcttaaaa tacatatctt tatttcaaga 180
tgacatttaa aaattattct aatatatcag cagcaaaaaa ataatttgca attacaaaaa 240
actaaactag aatccttaag ttattctcat gtttacagtt gtgattcttt aataaatact 300
attatgcagc tctattgttt aagctttctg gatttggttt aaacacatgc atatatattg 360
tcaattgtgg gaagctttac aagttatatt ccatgcactt ttggacaga gttctaacag 420
agccagccag tccacaaaac aggcaagaca aaagttgaat taactggggc aaaataggac 480
tcttatgcaa 490

```

&lt;210&gt; 104

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

cgtggtcgcg gccgaggtcc aggctggtct cgaactcctg accttgtgat ctgcccgcct 60
cgccctccca aagtgttggg attacaggca tgagccactg cgcccgaccg agttgaacat 120
ttaatgtcag actaggccag agtttctcaa tctttttatt ctacttccc aaaggagccg 180
ttggagattt tcccctcaat ctctctcctt catgaaattt cataccacaa atatagtatg 240
ttttatttat gtactgtgac cctttgaagg atcacaaacc aatataatag tttttctttt 300
taaccgcgca aggaccaagt ttttgccctc gttggaaatg cataaactgg actgatgaat 360
tggtatagat ggcttttatc atgaggatca gaaaaacttg aaattccttg gctacgacac 420
tccatattta tcaccgtata gggaggacct tggatatggg aagtagaaac acttctacac 480
tttacagca 489

```

&lt;210&gt; 105

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 142, 453

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 105

```

gcgtggctgc ggccgaggtc tgactggctt cagccccaga agttgagctg gcctttagac 60
aaaataattg cacctccctc tgctgcttat tcccttccgt ttttcatttg agtgatgaaca 120
gttagataaa atctgtggct gnetcttcca ccttgcctta gtttccattg ctgtgagcag 180
gccctcctat gccccgcatt tagctacaat gctgtggact cacttgattc ttttctccg 240
agctttgtct agaaatatgt gaaggtgagg ttaagtgtt ctctgtgtag atccacttag 300
ccctgtctgc tgtctcgatg ggcgttgctt cgtctctcct ctcttccatc ctttccattt 360
gcttctcacc accttctggc tttttttctt aatgcaataa aggcagtttc taacaaagaa 420
agaatgtggg ctttgaggtt agacagacct ggntttaaat tctgcttctg gctctccaa 479

```

&lt;210&gt; 106

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

```

tcggggccga ggtccaaaac gtggattcca atgacctgcc ttgagcccg c ggttgccagg 60
agttggacct gcagtagtat gggagctca cggcctaaat accgactgcc ctctgacccc 120
accgtccagc gattctagaa catcttctagt aggaaagaca tagcaaggga ttttcatgat 180
tgggaaatac tgggagacaa gctgaagatt tgtaagggc tatgcttctg tcatctttta 240
ggtattttaag gctactcctt tagctagcta ctttgagctg tttaaagtga ctatctccct 300
acacagagtt acacaatgag catctctgaa agagaatatt accctggatt tccaaagatg 360
tactctaaca ggatgaccag gcaaaagggtg acccggggga ggagtctgtt ataacactcg 420
gaccacatg ttctcaaggc acttcagaac tttgggaaat cattttgtac cggatcctca 480
gaaagcattt atggaaatac acatccttta g 511

```

&lt;210&gt; 107

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

```

ggccgcccgg gcaggtccag aatatcaaat caaaagggtca caaatgttca cttcctcctc 60
caccctctta catattggat cttcaattgc aatagggagt gtaagatggg catttttagag 120
acgtagtgtc atcagcagaa gcaaaccat cttatacaaa tgggttttgg ggataggaaa 180
aggctgctaa aaattcacaa gtcaccattc cccagaagca atgaatagcc gtagaagacc 240
aaggaagatc aacaagtctt caaagtgtc aagccagaga tttggccctt ccaaaatacc 300
accaggacgc ctggaccctg gggctctccg catgtcacca ctgactgcca ggatgctgct 360
gcacctccct tccttgagac acaacagaga gacagtgaag tcaccaaga ctgggatcat 420
cagaggctcc tcatgcttgc tacagagaag c 451

```

&lt;210&gt; 108

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

```

ccgcccgggc aggtcctgaa aacattcaga ctaatcaaaa tgggtactact gtaacttctt 60
ataatacata atataaaagt ttttgaaaga tatagacaca attaacccct aaacaacaca 120
ctatctgatt ctcaaaagca atggctattt aacaagatgt aaaaggacaa taacatatca 180

```

```
aagaactttc acacacctaa agatagcatt tagcagcaag ttagtcagac aaaacaaaca 240
caaataatattt cacatttcct atgtttgttt ttaactttac ttcataaagc cactgataat 300
tgaggtttct ttcaagtata agattttctaa aattaaaaac tgtttttgac atatttttat 360
aaagaaataa aaagcaaaac gcaatccaac tatttatatg agtccctctt ctccaacagc 420
tttagatggt tttctgagta cttttttaca cagaatattt t 461
```

&lt;210&gt; 109

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```
ggccgcccg ggcaggtctga ttataagaga aagaaatcca gtgacacgag ggcaggcagg 60
ccccgctctg ctctgatcga gaaaagcttc ctgatgtcag ggagatggaa ctgccaccat 120
cagaaccatg gcacttttgg tgaaggtgtg tcagcgacca agggggcagg aaatgggcag 180
tgactaaggg ggcaggaaac aggcaggcac atggcaagggt tctcccagcc catcagccca 240
gtgatggcct cgattttgaa gctgcactac tgtctgaaaa gcacaattac tgggtgactct 300
taacaaactt cagcactactg gggaaggaga ctgtcaagta actgaattgg aaagatgaaa 360
aagaaccatc tctaaaagt gatgcttgct agaagaataa cctcctttgt gcaagtcttg 420
caacatcttc attcaaccac a 441
```

&lt;210&gt; 110

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 260, 361

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 110

```
ggtcgcggcc gaggtctggg gaaggggtga gaatccctgg gccttgccca gtcctgagct 60
ctgggtgtct gcagggaagc acagtgtgtga gttagtgtta aagaaagcat ccagagaggt 120
aagaggggct tgggtagcac cctttgcctc tgtcacttcc gcaaaaactt cttgttgagg 180
aggaagatga gaaggttgac attgactttg gccttggtga agagtttcat gacagccaca 240
ccctcactact ggagctgcan gagatcctga tagtgaagct tgaaatcgct ccagtgtccac 300
acccaggaac ttggcattta cttcaaaactt tcctgcctca tctcccgcg tgatgtcaaa 360
natgacgttt cttgaagtga gaggcgggaa agatcttcaa tttccaccaa agacaccctt 420
tttcaggaa gcttgagcaa caagtgaat g 451
```

&lt;210&gt; 111

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

<222> 26, 33, 36, 79, 105, 111, 133, 149, 186, 206, 220, 239, 245,  
259, 336, 375, 383, 393

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 111

```
ggccgacgtt cgacctgact tctttngagc agntgncact acccgtcttg aggaatgccg 60
actgcagaca gtggcccang gcaaagagtg tgcgtcatcg atganattgg naagatggag 120
ctcttcagtc agnttttcat tcaagctgnt cgtcagacgc tgtctacccc agggactata 180
atcctnggca caatcccagt tcctanagga aagccactgn ctctttaga agaatcana 240
cacanaaagg atgtgaacng tgtttaatgt caccaaggga aaacatgaaa ccaccttctg 300
```

ccagatatcg ggacgttgcg tgcagatcaa gcacgnaagt gaagacgcgt gcatttccttg 360  
ccttccgtga acgantgccc agntcaagaa gancctgatg gaaccct 407

<210> 112  
<211> 401  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 363  
<223> n = A,T,C or G

<400> 112  
tcgcggccga ggtcggccga ggtctgacat ctgttgctctg tgataaccac ttctgtattg 60  
cgtcttaacc acttctgtat tgttggttt taactgccta aggcggcaat gggcagtggg 120  
cccctttccc ttaggatggg tatcaattca acaatattta taaggcattt actgtgtgct 180  
aagcatttg aagaccag ctacaaaata agacatagtt cctgccctcc aggcagcag 240  
agggaggcac aaataccag gaatctctga tgggtgtgaa gtgcggtcgt gggccacaga 300  
aaatgaccgt catggagacc ctgctaaagg tcggaccctg agcccaaagg ggtattcaga 360  
agnggagatg attttgccc cactcataga tgggtggcaa a 401

<210> 113  
<211> 451  
<212> DNA  
<213> Homo sapiens

<400> 113  
gtcgcggccg aggtccatat taaaaagtcc atcataaaca aagactcctc ctcatggtat 60  
gaatatgctc catatgccca taatggtgca taacggactt agaaattcca atgagtctta 120  
gggttgaaat ttccaatgac ctgagcaagg cagctccccta tagcttctgg ataacatttt 180  
acaccagag ttcaggctta aacagacctt tcaacacaat tattttcggg ttgtctgtct 240  
agaaaaacggc aatgctcaaa ggaatataaa taagggtggg gggacatatg cttccagcct 300  
ggcctttctc catgtggtaa aaaacaatgg aatggctgtg ttaatttttt ttaattcttt 360  
tctgaccttt actatgtttg gtaatggaaa taagtcaggg aaaacaaaat gaacaggtct 420  
catcacttaa ttaatactgg gttttcttct t 451

<210> 114  
<211> 441  
<212> DNA  
<213> Homo sapiens

<400> 114  
ggccgcccgg gcagggtccat cctgtcagag atgggagaag tcacagacgg aatgatggat 60  
acaaagatgg ttcaactttct tacacactat gctgacaaga ttgaatctgt tcatttttca 120  
gaccagttct ctggtccaaa aattatgcaa gaggaaggct agcctttaaa gctacctgac 180  
actaagagga cactgttgtt tacatttaat gtgcctggct caggtaacac ttacccaaag 240  
gatatggagg cactgctacc cctgatgaac atgggtgatt attctattga taaagccaaa 300  
aagttccgac tcaacagaga aggcaacaa aaagcagata agaaccgtgc ccgagtagaa 360  
gagaacttct tgaaacttga cacatgtgca aagacaggaa gcagcacagt ctcggcggga 420  
ggaagaaaaa aagaacagag a 441

<210> 115  
<211> 431  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc\_feature  
<222> 317  
<223> n = A,T,C or G

<400> 115  
gcccgcggg caggtccatt ggccgtgaca aaaggaaaag aagcaaagag actcagtcca 60  
taatgctgat tagttagaag aaagggctag gattgagaaa gtaccaggaa cttttaatta 120  
tttaaaagag aatgctgact gttaatgttt taaatcttac tgttcaaag tactaatatg 180  
aatttttacc ctttgtgcat gaattattcta aacaactaga agacctccac aatttagcag 240  
ttatgaaagt taaacttttt attataaaaa ttctaaacct tactgtctct ttaccaggaa 300  
catgacacac tatttancat cagttgcata cctcgccaat agtataattc aactgtcttg 360  
cccgaacaat catctccatc tggaagacgt aagcctttag aaacacattt ttctattaat 420  
ttctctagaa c 431

<210> 116  
<211> 421  
<212> DNA  
<213> Homo sapiens

<400> 116  
gtcgcggccg aggtccagaa atgaagaaga agtttgcaga tgtatttgca aagaagacga 60  
aggcagagtg gtgtcaaatc tttagacggca cagatgcctg tgtgactccg gttctgactt 120  
ttgaggaggt tgttcatcat gatcacaaca aggaaccggg gctcgtttat caccagttag 180  
gagcaggacg tgagcccccg ccctgcacct ctgctgttaa acacccagc catcccttct 240  
ttcaaaaggg atcctttcat aggagaacac actgaggaga tacttgaaga atttggaattc 300  
agcccgcgaa gagatttatc aagcttaact cagataaaat cattgaaagt aataaggtaa 360  
aagctaagtc tctaacttcc aggccccagc ctcaagtga tttcgaatac tgcatttaca 420  
g 421

<210> 117  
<211> 489  
<212> DNA  
<213> Homo sapiens

<400> 117  
agcgtggtcg cggccgaggt aaggctgcga ggttgtggtg tctgggaaac tccgaggaca 60  
gagggctaaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 120  
ctactacgtt gacactgctg tgcgccacgt gttgctcaga cagggtgtgc tgggcatcaa 180  
ggtgaagatc atgctgcctt gggacccaac tggtaagatt ggccctaaga agcccctgcc 240  
tgaccacgtg agcattgtgg aaccctaaaga tgagatactg cccaccaccc ccattctcaga 300  
acagaagggt gggaaagccag agccgcctgc catgccccag ccagtcccca cagcataaca 360  
gggtctcctt ggagacactg cccgggcggc cgctcgaaag cccgaattcc agcacactgg 420  
cggccgttac tagtggtacc cagctcggtg ccaagcttgg cgtaatcatg gtcatactg 480  
gtttcctgt 489

<210> 118  
<211> 489  
<212> DNA  
<213> Homo sapiens

<400> 118  
tcgagcggcc gcccgggcag gtattgaata cagcaaaatt ctatatataa agtgacctgg 60  
acctgctgct tcaaaacatg atcctttctt actaatatct tgatagtcgg tccatagagc 120  
attgaaaagc aattgactct taaataaaca gaaaagtgcc taatgcacat taaatgaatg 180  
gcctaactac tggaaacttta gtagttctat aagggtgatta acataggtag gatccagttc 240  
ctatgacagg ctgctgaaga acagatatga gcatacaag gccattttgt gcactgccac 300  
cgtgatgcca tcgtgtttct ggatcataat gttcccatta tctgattcta gacacaccac 360  
aggaatatca gtggggtcag aggttagctt agctgcttgc tgggctagaa cagatatcac 420

tccagcatgc tcacttgaca gggccccgcg gcaaccacaga ttaagtcctt gtgaatctgt 480  
gcacaggga 489

<210> 119

<211> 181

<212> DNA

<213> Homo sapiens

<400> 119

taggttccag agacttttgg cccaggagga atatttactt ttagctctgg acatcattac 60  
aaaaaggaat atttcccaaa cctcttcaga ccgagaatac atgggtaaaa ttattaaata 120  
gttgataaat aaaaataatt ttttccttaa aaaaaaaaaa aacctcggcc gcgaccacgc 180  
t 181

<210> 120

<211> 489

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 422, 487

<223> n = A,T,C or G

<400> 120

gcgtgggtgc ggccgaggtc catttaaaac aaagaaaaat actaaagcca ctagtaaaaca 60  
tctgatgtgc aaaatacaac atcctctagt tggctttatg ccattattac ataagctcca 120  
aatagctcat cttaaattaa aaagaaaaag tggctgtccc atctctgctg cataaatcag 180  
atTTTTTTTT aaaggTTtag agtactTTaa ggaagggaag ttcaaaaactg ccagtgaat 240  
tcacagagaa tacaaattta gcaatttaat ttcccaaagc tctttgaaga agcaagagag 300  
tctctcttct taatgcagtg ttctcccaag aggaactgta attttgcttg gtacttatgc 360  
tgaggagatat gcaaaatgtg tttttcaatg ttgtctagaa tataatggtt cctcttcagt 420  
gnctgggtca tcctggaact catgggttaa gaaggacttc ttggagccga actgcccggg 480  
cgggccntt 489

<210> 121

<211> 531

<212> DNA

<213> Homo sapiens

<400> 121

cgagcggccg cccgggcagg tggccagcgc tgggtcccga gacgccgaga tggaggaaat 60  
atttgatgat gcgtcacctg gaaagcaaaa ggaaatccaa gaaccagatc ctacctatga 120  
agaaaaaatg caaactgacc gggcaaatag attcgagtat ttattaaagc agacagaact 180  
ttttgcacat ttcattcaac ctgctgctca gaagactcca acttcacctt tgaagatgaa 240  
accagggcgc ccacgaataa aaaaagatga gaagcagaac ttactatccg ttggcgatta 300  
ccgacaccgt agaacagagc aagaggagga tgaagagcta ttaacagaaa gctccaaagc 360  
aaccaatgtt tgcactcgat ttgaagactc tccatcgtat gtaaaatggg gtaaaactgag 420  
agattatcag gtcccagagga ttaaactggc tcatTTcttt gtatgagaat ggcatacatg 480  
gtatccttgc agatgaaatg ggcctaggaa agactcttca acaatttctc t 531

<210> 122

<211> 174

<212> DNA

<213> Homo sapiens

<400> 122

tcgagcggcc gcccgggcag gtctgccaac agcagaggcg gggcctccgg catcttcaaa 60

gcacctctga gcaggctcca gccctctggc tgcgggaggg gtctggggtc tcctctgagc 120  
tcggcagcaa agcagatggt atttctctcc cgcgacctcg gccgcgacca cgct 174

<210> 123  
<211> 531  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 152, 373, 482, 494, 496, 502  
<223> n = A,T,C or G

<400> 123  
agcgtggtcg cggccgaggt cctcaaccaa gagggttgat ggcctccagt caagaaactg 60  
tggtcatgca cagcagagct ctctcctcgt ccagcaggcg ccatgcaagg gcaggctaaa 120  
agacctccag tgcatacaaca tccatctagc anagagaaaa ggggcaactga agcagctatg 180  
tctgccaggg gctaggggct cccttgcaaga cagcaatgct acaataaagg acacagaaat 240  
gggggaggtg ggggaagccc tatTTTTata acaaaagtcaa acagatctgt gccgttcatt 300  
ccccagaca cacaagtaga aaaaaaccaa tgcttggtgt ttctgccaag atggaatatt 360  
cctccttcct aanttcacaca catggccggt tgcaatgctc gacagcattg cactgggctg 420  
cttgtctctg tgggtctggc accagtagct tgggccccat atacacttct cagttcccac 480  
angccttatg gccnangggc angctccaat tttcaagcac cacgaaggaa g 531

<210> 124  
<211> 416  
<212> DNA  
<213> Homo sapiens

<400> 124  
tcgagcggcc gcccgggcag gtccatctat actttctaga gcagtaaact tcataaattc 60  
acttaccaag cccaggaata atgactttta aagccttgaa tatcaactaa gacaaattat 120  
gccaatctctg atttctcaca tatacttaga ttacacaaag ataaagcttt agatgtgac 180  
attgtttaat gtagacttat ctttaaagtt ttttaattaaa aactacagaa gggagtaaac 240  
agcaagccaa atgatttaac caaatgattt aagagtaaaa ctactcaga aagcattata 300  
cgtaactaaa tatacatgag catgattata tacatacatg aaactgcaat tttatggcat 360  
totaagtaac tcatttaagt acatttttgg catttaaaca aagatcaaat caagct 416

<210> 125  
<211> 199  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 112, 160, 195  
<223> n = A,T,C or G

<400> 125  
agcgtggtcg cggccgaggt gctTTTTttt tttttttttt tttttttttt gctattctaa 60  
aggggaaggc ccctttttat taaacttgta cattttactt tccttctttc anaatgctaa 120  
taaaaaactt ttgtttatac ttaaaaaaac cataaatcan acaaacaaaa gaaacgatc 180  
caacatcact tctgngatg 199

<210> 126  
<211> 490  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 126

```
cgtggtcgcg gccgaggtcc agttgctcta agtggattgg atatggttgg agtggcacag 60
actggatctg ggaaaacatt gtcttatttg cttoctgcca ttgtccacat caatcatcag 120
ccattcctag agagagggcga tgggcctatt tgtttggtgc tggcaccaac tcgggaactg 180
gccaacacagg tgcagcaagt agctgctgaa tattgtagag catgtcgctt gaagtctact 240
tgtatctacg gtggtgctcc taagggacca caaatcgtg atttggagag aggtgtgga 300
atctgtattg caacacctgg aagactgatt gacttttttag agtgtggaaa aaccaatctg 360
agaagaacaa cctaccttgt ccttgatgaa gcagatagaa tgcttgatat gggctttgaa 420
ccccaataa ggaagattgt ggatcaaata agacctgata ggcaaaactct aatgtggagt 480
gcgacttggc 490
```

&lt;210&gt; 127

&lt;211&gt; 490

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

```
cgtggtcgcg gccgaggtcg gccgaggtct ggagatctga gaacgggcag actgcctcct 60
caagtgggtc cctgaccctt gaccccccag cagcctaact gggaggcacc cccagcagg 120
ggcacactga cacctcacac ggcaggggat tccaacagac ctgaagctga gggctcctgtc 180
tggttagaagg aaaactaaca agcagaaagg acagccacat caaaaaccca tctgtacatc 240
accatcatca aagaccacaaa gtaaatataa ccacaaagat gggaaaaaaaa cagaacagaa 300
aaactggaaa ctctaaaaag cagagcacct ctctcttccc aaaggaacgc agttcctcac 360
cagcaatgga acaaagctgg atggagaatg actttgacga gctgagaaaa gaacgcttca 420
gacgatcaaa ttactctgag ctacgggagg acattcaaac caaaggcaaa gaagttgaaa 480
actttgaaaa 490
```

&lt;210&gt; 128

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 69, 106, 140, 152, 165, 196, 224, 233, 241, 258, 260, 267, 291, 347, 395

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 128

```
cgtggtcgcg gccgaggtgc tttttttttt tttttttttt tttttttttt tgctgattta 60
ttttttctnt ttattgttac atacaatgta taaacacata aaacanaaaa cagtagggat 120
cctctaggat ctctagggan acagtaaagt anaaagaggt ctcanaaaca ttttttttaa 180
gtacaagaca ttcagngctc ggcccaaagg cgtaaaaggt ttanagccag canatagctg 240
nactaaaggc tccgtctntn tccccanagc caggacaacc ccaggggagct ntccattagc 300
agccagtcca cgcaggcagg atgctgcgga aaaagctcta tgctganaac attccccttg 360
atggaaagaa gggcaacaca aaaggggtaa ctaanagctc cttcctctcg tgagggcgac 420
aactgaggaa cagaaaagga gtgtcccatg tcacttttga cccctctccc 469
```

&lt;210&gt; 129

&lt;211&gt; 419

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

```
gcgtggtcgc ggccgaggtc tgattttcat ttaaatattt cagagctata gcatttgcct 60
ccatgtctaa atccacacca ttggggctta agccgctcat gccaacatta gcaaatgaca 120
tgcagtttaa tccagagatc actgcttctg ggctgatgca tgccaacaca ctggcgctgat 180
```

```

ccacgttatg tgcatttttc ttcacttttag tgggagaatc aatttttact ccaaggcttc 240
ttagttgctt aagagttgca ttaaggacac aatctttgtc caccagtctt gaatgatgtg 300
tttttttctt tgtatggtaa acgttttggg ttctgggtgca ttcagtactg ataattactg 360
ctttggtaga cggtctgtca agtttccttg gaggaactat ttaatagggtg ggttacttg 419

```

<210> 130

<211> 354

<212> DNA

<213> Homo sapiens

<400> 130

```

agcgtggtcg cgcccgaggt ccatctgagg agataaccac atcactaaca aagtgggagt 60
gaccccgagc agcacgctgt ggaattccat agttggtctc atccctgggc agtttccaca 120
tgatgatggg ctatatctga gaggcggaga ggatcatgtc cggaactgac ggggtagtag 180
cgatctgggt taccagccg ttgtggccct tgagggtgcc acgaagggtc atctgctcag 240
tcatggcggc ggcgagagcg tgtgtcgtcg cagcgacgag gatggcactg gatggcttag 300
agaaactagc accacaacct ctctgcgcgc acctgccggg gcggcccgcg cgaa 354

```

<210> 131

<211> 474

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 421

<223> n = A,T,C or G

<400> 131

```

cgagcggccg cccgggcagg tctggcagca gcttcctctg gaataattga cagctttgtg 60
ctgcctgact aaaatttgaa atgacaaccg ctgaatgtaa aatgatgtac ctacaatgag 120
agagatttag gaatactatc tgtcaatcca tagatgtaga aacaaaacaa actacagaat 180
gaaaacaaac ttattttaaa ccaaagaaac aaatgtatcc aaaatatagt ccatgatata 240
tttgattact agtataacca cagttgaaaa cttaaaaaaa aaaattgaca ttttttgtaa 300
tgggtactaa tggatttata aaagggttct gtttccaaag atgttattgg ggtccacata 360
ttccttgaag acttcagcat cccaagccc gacatcagag ataacttctt ttagccattg 420
nttcccgtaa cttgcccaact ccatggtgat gtgacagget tcccttcatt agca 474

```

<210> 132

<211> 474

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 403

<223> n = A,T,C or G

<400> 132

```

ggccgaggtg ggggaattcat gtggaggtca gagtggagc aggtgtgaga gggccagca 60
gaaggaaaca tggctgccaa agtgtttgag tccattggca agtttggcct ggccttagct 120
gttgaggagc gcgtggtgaa ctctgcctta tataatgtgg atgctgggca cagagctgtc 180
atctttgacc gattccgtgg agtgcaggac attgtggtag ggggaaggac tcattttctc 240
atcccgtggg tacagaaacc aattatcttt gactgccgtt ctgcaccacg taatgtgcca 300
gtcatcactg gtagcaaaaga tttacagaat gtcaacatca cactgocgat cctcttccgg 360
cctgtcgcca gccagcttcc tcgcatcttc accagcatcg ganaggacta tgatgaaccg 420
tgtgctgcgc tccatcacaa ctgagatcct caagtcagtg gtggtcgcgt ttga 474

```

<210> 133  
<211> 387  
<212> DNA  
<213> Homo sapiens

<400> 133  
tgctcgagcg gccgccagtg tgatggatat ctgcagaatt cggcttagcg tggctcgggc 60  
cgaggtctgc gggcccctta gcctgccctg cttccaagcg acggccatcc cagtagggga 120  
ctttcccaca ctgtgccttt acgatcagcg tgacagagta gaagctggag tgcctcacca 180  
cacggcccgg aaacagcggg aagtaactgg aaagagcttt aggacagctt agatgccgag 240  
tgggcgaaatg ccagaccaat gatacccaga gctacctgcc gccaaacttg tgagatgtgt 300  
gtttgactgt gagagagtgt gtgtttgtgt gtgtgtttt ccatgaactg tggccccagt 360  
gtatagtgtt tcagtggggg agaactg 387

<210> 134  
<211> 401  
<212> DNA  
<213> Homo sapiens

<400> 134  
ggccgcccgg gcaggtctga tgaagaacac ggggtgtgatc cttgccaatg acgccaatgc 60  
tgagcggctc aagagtgttg tgggcaactt gcatcggctg ggagtcacca acaccattat 120  
cagccactat gatggggcggc agttcccaca ggtggtgggg ggctttgacc gagtactget 180  
ggatgctccc tgcagtggca ctgggggtcat ctccaaggat ccagccgtga agactaaca 240  
ggatgagaag gacatcctgc gcttgtgctc acctccagaa ggaagtgtct cctgagtget 300  
attgactctt gtcaatgcga ccttcaagac aggaggctac ctggtttact gcacctgttc 360  
tatcacagtg agacctctgc catggcagaa cagggaagc t 401

<210> 135  
<211> 451  
<212> DNA  
<213> Homo sapiens

<400> 135  
ggtcgcgggc gaggtctgtt cctgagaaca gcctgcattg gaatctacag agaggacaac 60  
taatgtgagt gaggaagtga ctgtatgtgg actgtggaga aagtaagtca cgtggggcct 120  
tgaggacctg gactgggtta ggaacagtgt tactttcaga ggtgaggtgt cgagaaggga 180  
aagtgaatgt ggtctggagt gtgtccttgg ccttggctcc acagggtgtg ctttccctctg 240  
ggcccgctcag ggagctcatc ccttgtgttc tgccaggggtg gggtagcggg gtttgacact 300  
gaggagggta acctgctggc tggagcggca gaacagtggc cttgatttgt cttttggaag 360  
attttaaaaa ccaaaaagca taaacattct ggtccttcac aatgctttct ctgaagaaat 420  
acttaacgga aggacttctc cattcaccat t 451

<210> 136  
<211> 411  
<212> DNA  
<213> Homo sapiens

<400> 136  
ggccgcccgg gcaggtctga atcacgtaga atttgaagat caagatgatg aagccagagt 60  
tcagtatgag ggttttcgac ctgggatgta tgtccgcgtt gagattgaaa atgttccctg 120  
tgaatttgtg cagaactttg acccccttta cccattatc ctgggtggct tgggcaacag 180  
tgagggaaat gttggacatg tgcagggtggg tccctttgct gcgtatttgg tgcctgaggc 240  
tctgtggatt tcccctccat caatcatctt accctctcat cccctcaga tgcgtctgaa 300  
gaaacatctc tgggataaga aaatcctcaa gtcccaagat ccaatcatat tttctgtagg 360  
gtggagggaag tttcagacca tcctgctcta ttatatccga agaccacaat g 411

<210> 137

<211> 211  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 186  
<223> n = A,T,C or G

<400> 137  
cggccgccg ggcaggtcgg ttggtgcggc ctccattggt cgtgttttaa ggcgccatga 60  
ggggtgacag aggcgtggt cgtggtgggc gctttggttc cagaggaggc ccaggaggag 120  
ggttcaggcc ctttgaccca catatcccat ttgacttcta tttgtgtgaa atggcctttc 180  
cccgnntcaa gccagcacct cgatgaaact t 211

<210> 138  
<211> 471  
<212> DNA  
<213> Homo sapiens

<400> 138  
gccgccggg caggtctggg ctggcgactg gcatccaggc cgtaactgca aatctatgct 60  
aggcggggtc tcccttctgt gtgttcaagt gttctcgact tggattctta actattttta 120  
aaaatgcact gagtttgggt taaaaaccaa ccacaaaat ggatttcaac acagctctaa 180  
agccaagggc gtggccggct ctcccaacac agcgactcct ggaggccagg tgcccatggg 240  
cctacatccc ctctcagcac tgaacagtga gttgattttt ctttttataa taaaaaaagc 300  
tgagtaatat tgcataggag tacciaaгаа ctgcctcatt ggaaacaaaa actatttaca 360  
ttaaataaaa agcctggccg caggctgcgt ctgccacatt tacagcacgg tgcgatgcac 420  
acggtgacca aaccacggag gcaagcttct ggcactcaca ccacgaccg c 471

<210> 139  
<211> 481  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 384  
<223> n = A,T,C or G

<400> 139  
gtcgcggccg aggtctgttc tttagctcag atttaaacct gctgtctctt ctttatttgc 60  
agaatgaatt cccagttcct gagcagttca agaccctatg gaacgggcag aagttgggtca 120  
ccacagtgc agaaattgct ggataagcga agtgccactg ggttctttgc cctcccttca 180  
caccatggga taaatctgta tcaagacggg tcttttctag atttctctta cctttttgct 240  
cttaaaactg cttctctgct ctgagaagca cagctacctg ccttactga aatataacct 300  
aggctgaaat ttgggggtgg atagcaggtc agttgatctt ctgcaggaa gtgcagcttt 360  
tccatatcag ctcaaccacg ccgncagtc attcttaagg aactgccgac taggactgat 420  
gatgcatttt agcttttgag cttttggggg gtattctacc aaccaacagt ccatttggaa 480  
a 481

<210> 140  
<211> 421  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

&lt;222&gt; 372

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 140

```

gtcgcgggccg aggtttccca ttttaagaaaa atagatcttg agattctgat tcttttccaa 60
acagtccctt gctttcatgt acagcttttt ctttacctta cccaaaattc tggccttgaa 120
gcagttttcc tctatggctt tgccctttctg attttctcag aggctcgagt ctttaataata 180
accccaaatg aaagaaccaa ggggaggggt gggatggcac ttttttttgt tggctctgtt 240
ttgttttgtt ttttggttgg ttgggttccg ttatttttta agattagcca ttctctgtgt 300
ctatttccct acataatgtc aatttttaac cataattttg acatgattga gatgtacttg 360
aggctttttt gntttaattg agaaaagact ttgcaatttt ttttttagga tgagcctctc 420
c

```

421

&lt;210&gt; 141

&lt;211&gt; 242

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 4, 6, 20, 31, 35, 39, 72, 94, 141, 142, 211, 222

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 141

```

cgantngccc gcccgggcan gtctgtctaa ntttntcang gaccacgaac agaaactcgt 60
gcttcaccga anaacaatat cttaaaccatc gaanaattta aatattatga aaaaaaacat 120
tgcaaaatat aaaataaata nnaaaaggaa aggaaacttt gaaccttatg taccgagcaa 180
atccaggtct agcaaacagt gctagtccta nattaacttga tntacaacaa cacatgaata 240
ca

```

242

&lt;210&gt; 142

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; 15, 19, 32, 73, 110, 278, 405, 436, 473, 510

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 142

```

agcgtggtcg cggcncgang tccacagggc anatattctt ttagtgtctg gaattaaaat 60
gtttgagggt tangtttgcc attgtctttc caaaaaggcca aataattcan atgtaaccac 120
accaagtgca aacctgtgct ttctatttca cgtactgttg tccatacagt tctaaataca 180
tgtgcagggg attgtagcta atgcattaca cagtcgttca gtcttctctg cagacacact 240
aagtgatcat accaacgtgt tatacactca actagaanat aataagcttt aatctgaggg 300
caagtacagt cctgacaaaa gggcaagtgt gcataataga tcttcgatca attctctctc 360
caagggggccc gcaactaggc tattattcat aaaacacaac tgaanagggg attgggttta 420
ctggtaaate atgtgntgct aaatcatttt ctgaacagtg ggggtctaaat cantcattga 480
tttagtgga gccacctgcc cggcggccgn tcgaagccca attctgcaga tatccatcac 540
actggcggcc g

```

551

&lt;210&gt; 143

&lt;211&gt; 515

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature  
<222> 5, 286, 498  
<223> n = A,T,C or G

<400> 143  
cgagngggccc gcccgggcag gtatcttcac aaactcaaca aaggcactac atgagacttc 60  
acattccccct agtccaatag ctgacaaatt tttgcaacgt tctgcaatgc gaattaactc 120  
ttcatcaagt ggccgtaatc catttgacaca cactactagt tcaaccagtc tagggcatgt 180  
cattcccaca cgcccaagca catctttgct tactgatctc ccaaagtaca gatgggtggc 240  
aggtatttca tagcgaaga aggggtcaaa ttcttcttca tataanaaaa aatacatcac 300  
taagttcact ttgggtgaat gtctgatgaa agcatcccag ctactcttct gaatagtatg 360  
gaagtgtgtc tgtccaggat tctcactgac tacatcaatg cgcaaatgtt ctaatcgaac 420  
atgtttttca gaagacaatg caagtaacaa ctcactcctc aataagtggg aagttcaggg 480  
ctagttctct taagccgnga cactgatcag cacac 515

<210> 144  
<211> 247  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 11, 20, 42, 115, 152, 165, 181, 195, 208, 221  
<223> n = A,T,C or G

<400> 144  
tgcattctct ntggatgcan acctgccctg tggtagggac tntgctcaca cggaacatgg 60  
acggttacac ctgtgccgtg ggtgacgtcc accagcttct ggatcatctc ggcnggggtg 120  
ttgtggaagg gcagactatc cacctccatg cncacgatgc ccganacgcc actccggact 180  
ntgtgctgca ccaanatgcc cagcatnta tcttcaagca naggcattat cagggctcctt 240  
ggcacac 247

<210> 145  
<211> 309  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 18, 155, 247  
<223> n = A,T,C or G

<400> 145  
cgtgggtcgc ggcccgangt ctgctgtaac aaaacaccat agtctgggca gctcatagac 60  
aatggaattt tatttctcac gcttctggag gctggattcc aagatcaagg ttccaggaga 120  
ctcagtgtct ggcaaggctc cggtttctgc ctcanagatg gtgccatctg gctgtgtcct 180  
cacaagtagg aaggtgcaag aagctccctc caggctctgt ctgtaagaca ctgatcccat 240  
tcattganggg gaaacgtaat gacctaatca gccccagag accccacttc taacaccatc 300  
accttgggg 309

<210> 146  
<211> 486  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 16, 97, 154, 244, 275, 322, 347, 349, 352, 357, 449, 460,

472

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 146

```
agcgtgggtc gcggnccgac gtcctgtcca tatttcacag cccgagaact aatacaagat 60
gttgacatca tttttgtcc ctacaactat cttctanatg cacaataag ggaaagtatg 120
gatttaaate tgaaagaaca ggttgtcatt ttanatgaag ctcataacat cgaggactgt 180
gtcggggaat cagcaagtta cagtgtaca gaagttcagc ttcggtttgc tcgggatgaa 240
ctanatagta tggtaacaa taatataagg aaganagatc atgaaccctt acgagctgtg 300
tgctgtagcc tcattaattg gntagaagca aacgctgaat atcttgnana angagantat 360
gaatcagctt gtaaaatatg gagtggaat gaaatgctct taactttaca caaaatgggt 420
atcaccactg ctacttttcc ctttttgcng gtaagatatn ttttctacct gngaaacgta 480
tttaag 486
```

&lt;210&gt; 147

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 13, 26, 28, 289, 299, 352, 390, 399

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 147

```
gccgcccggg cangttcgac attacntnga gttccatgat gtacaattct ttcacgaaaa 60
acaatgaatg caagaatttg aggatctcct tactcctccc ttttacagat ggtctctcaa 120
tcccttcttc ttctcttca tcttcatctt ctcttgaacg cgctgccggg taccacggct 180
ttctttgtct ttatcgtgag atgaagggtg tgcttctgtt tcttctacca taactgaaga 240
aatttcgctg caagtctctt gactggctgt ttctccgact tcgcctttnt gtcaaacng 300
agtcttttta cctcatgccc ctccagcttca cagcatcttc atctggatgt tnatttctca 360
aagggtcac tgaggaaact tctgattcan atgtcgaana gcactgtgaa gttttctctt 420
cattttgctg 430
```

&lt;210&gt; 148

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 20, 24, 53, 55, 374, 381, 423, 431, 459

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 148

```
cccgggcagg tctgtgttgn tttncacccg gtgtcctccc cagcgtccag aananggaaa 60
tgtggagcgg gtgatgatga cccctcgtg tcctgtcacc tcctgcacag cttcgtatgt 120
gggtctggtc tgggaccacc cgtacagggt gtgcacgttg tagtgctcca cgggggagct 180
gtccggcagg atctgctgac tctccatgca cagagtcttg ctgtcaggc ccttgtccct 240
agattccaaa tatggcatat aggggtgggt tatitagcat ttcatgtctg cagccctga 300
cagatccatc cacaaaattt gatggctcat tcatatcaat ccacaatcca tcaaacttca 360
agctcttctc tggntctcga nggtttgcat agaactcttc tatctctttc ttccaccacg 420
canacctcgg ncgcgaccac gctaagccga attctgcana tatccatcac actggcggcc 480
gct 483
```

&lt;210&gt; 149

&lt;211&gt; 439

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 11, 359, 384, 402

<223> n = A,T,C or G

<400> 149

```
ctttcacgaa nacaatgaat gcaagaattt gaggatctcc ttactcctcc cttttacaga 60
tgggtctctca atcccttctt cttcctcttc atcttcatct tcttctgaac gcgctgccgg 120
gtaccacggc tttctttgtc tttatcgtga gatgaagggt atgcttctgt ttcttctacc 180
ataactgaag aaatttcgct gcaagtctct tgactggctg tttctccgac ttcgcctttt 240
tgcaaacgtg agtcttttta cctcatgccc ctacgcttcc acagcatctt catctggatg 300
ttcattttctc aaagggtca ctgaggaaac ttctgactca catgtcgaag aagcactgng 360
agtttctctt catttgctgc aaanttgtct tttgctggct gngctctcag accacccatt 420
tggctgcatg ggggctgac                                     439
```

<210> 150

<211> 578

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 4, 15, 260, 336, 371, 430, 461, 535, 572

<223> n = A,T,C or G

<400> 150

```
ggcncgcccg ggcangtcca ctccactttt gagctctgag ggaatacctt caggagggac 60
agggtcaggg agtcctggca gctccgcagc agagattcac attcattcag agacttggtg 120
tccagtgcaa tgccattgat cgcaacgatc ctgtctccca cagcaaggga cccttcttta 180
gcggcagggc ttccaggcag cacagcggca gcatacactc cattctccag actgatgcca 240
ctgtctttct gtccactgan gttgatgtgc agcggcgtga ccacottccc acccagggac 300
ttcctccgcc gcacgaccat gttgatgggc cccctnccca ttgaggagcg ccttgatggc 360
ctgcttcttg nccttgggtga tgaagtccac atcggtgatt ctacagacca gtcattgacc 420
cttaagcggg catcagcaat gcttcttttg gccactttag ngacaaatat gccacagtcc 480
ccgggaaaca agggtcattc acaccttctg gcataatcaa cacctcggcc gggancacta 540
agccgaattc tgcagatatc catcacactg gngggccg                                     578
```

<210> 151

<211> 503

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 392, 464

<223> n = A,T,C or G

<400> 151

```
cgagcggccc gcccgggcag gtctgggaga tcagcgactg ctgccacgtg cccagaaatg 60
gctcgtcctt tcaactacagc ggaatgcaat gagggtgggt gagaagatga tgggtcgggt 120
atttcattcc ttttcttttt acaacttcac tttcagagac ttcagcgttc catgtctgct 180
gtgctgtgga acccagagtg ctcttgccctg gatggctgag aatcccttgg accctggaag 240
cacctactcc atgatggccc ggtatagtgc aggcctcaata taatcttccc ggtatottga 300
gttgataaact cgttgccgtt tcttttcttg cttaacctct ttctctgtga aaatctcatt 360
gaagcgcagc tctgaagcta ctgacagtct anatttgact ctcttgggaa gctcttcatt 420
cagtgtgtat acatcatctc tcttaaccac aagttggagc catncttaaa cttcacctgg 480
```

tacatttgga taggggtggga ggc

503

&lt;210&gt; 152

&lt;211&gt; 553

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 293, 432, 459, 481, 536

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 152

```
agcgtgggtcg cggccccgagg tccactgagc tccgccttcc ccggggtccc tgaggaagca 60
gagtcctgac ttccagggaag gacaggacac agaggcaaga actcagcctg tgaggctctg 120
ggtggctcct gaggccagag gacgccttcc gcgatccatg gctcagcatc gtccttctgg 180
cttcccagcc ccgggcccga cgttcgggtt aataagcaga gcagttattc ggctcctggc 240
aggagctccc ccgttagttt ccacgttggt agcacattca tacttaagac tgnttctctt 300
tgtgttttaa gcgtctgtct ctgtagtaaa ctgaaatgtt aacagaaatg cagacctgcc 360
cgggcggccg ctcgaaagcc gaattctgca gatatccatc acactggcgg ccgctcgagc 420
atgcatctag anggcccaat tcgccctata gtgagtcgna ttacaattca ctgggcccgcg 480
ntttacaacg tcgtgactgg gaaaaccctg cggtaaccac ttaatcgctt tgcagnacat 540
ccccctttcg cca
```

&lt;210&gt; 153

&lt;211&gt; 454

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 198, 307, 325, 347, 386, 389, 392, 415, 425

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 153

```
tcgagcggct cgccccggca ggtccaccta gcatggctcc tctaaacacg caactcagcg 60
aggggacccc cttcacctct ggcaagagag ctgggtagat cagaaacttg gtgacacctg 120
gctagcacag agcaggctca cttgtcttgg tcccactacc cagattcctg cagacattgc 180
aaaccaaattg aaggttgntg aatgacccct gtccccagcc acttgttttg gtatcatctg 240
ctctgcagtg gaatgcctgt gtgtttgagt tcaactctgca tctgtatatt tgagtataga 300
aaccgantca agtgatctgt gcatncagac aactggggc acctgancac agaacaaatc 360
accttaacga tctggaatga aactgnganc antgcccgcg tgggtgggtc tgganaaact 420
gccgncttct tgttggacct tggccgcacc acct
```

&lt;210&gt; 154

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 19, 33, 37, 131, 377, 425, 439, 505

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 154

```
agcgtgggtcg cggccccgang gcggcctcct gantganggg aagggacgtg ggggcccggca 60
cggcaggatt aacctccatt tcagctaata atgggagaga ttaaagtctc tcctgattat 120
aactggttta naggtacagt tccccctaaa aagattattg tggatgatga tgacagtaag 180
```

```

atatggtcgc totatgacgc gggccccga agtatcaggt gtcctctcat attcctgccc 240
cctgtcagtg gaactgcaga tgtctttttc cggcagattt tggctctgac tggatggggg 300
taccgggtta tcgcttttga gtatccagtt tattgggacc atctcgagtt ctgtgatgg 360
attcacaaaa cttttanacc atttacaatt ggataaagtt catctttttg gcgtttcttt 420
gggangcttt ttggcccaana aatttgctga atacactcac aaatctccta gaagccattc 480
cctaattctc tgcaattcct tcagngacac ctctatcttc aaccaacttg gactggaaac 540
agctttgggt gatgcctgca tttatgctca aaaaatagtt ctgggaaatt ttcata 596

```

&lt;210&gt; 155

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 6, 12, 23, 44, 58, 86, 99, 279, 310, 319

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 155

```

ctcganttgg cncgcccggg cangtctgcc tggtttttga ccngcgcgagc tatttagtct 60
ctggctctgt ttccggagct caaggnaaaa atcttgaana actcgagcag cttctgtgga 120
tagccttggg tacacatact gccgagcata gccaatgtac tttctcaata gctgggtggg 180
aatgggatct attgtttctc caggaaccac ctttagtctt tctgataatg gcttctcaga 240
aactacttca agtacggaag tatttgaatc ttgactatnc atacgagcta ctgtggcact 300
gctaattggg tctctgctnt ccagctctta ttgcaatcac atg 343

```

&lt;210&gt; 156

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 34, 375, 530

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 156

```

tcgagcggcc cgcccgggca ggtctggcac cacncagatc gattaactgg ctcatctgat 60
ctcgtggccc ccacctgga actgacttag cacaaaagga cacctcaatt cttatgatt 120
tcatctccga cccaaccaat caacaccctt gactcactgg ccttccccct cccaccaa 180
tattcttaaa aactctgac cccgaatgct caggagatc gatttgagta ctaataagac 240
tcagctctcc tgcacaagca gctctgtgta ctcttctctt attgcaattc ctgtcttgat 300
aaatcggtc tgtgtaggcg gcggaagaag tgaacctgtt gggcggttac cacctctgtc 360
gtgtgtgaca gttgntttga atctctaatt gctcagtaca gatccacatg caggttaagt 420
aagaagcttt tgaagaaaat ggaaagtctt aagtgatggc ttccaagaaa tcaaacctac 480
attaattagg gaacaacgga ctttacgtat cacaaatgaa gagactgacn aagtaaatca 540
acttggcctt ttctta 556

```

&lt;210&gt; 157

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 18, 40, 55, 57, 60, 91, 97, 103, 110, 161, 173, 193, 195,

196, 214, 231, 233, 238, 263, 264, 266, 283, 284, 287, 297,

298, 323, 331

<223> n = A,T,C or G

<400> 157

```
ggtccacaaa aatatatnaa ataagctgga tatataaaan caaacactta acatngncaan 60
cattccttca gttattcaaa ctcactgata nctaacnggg agnagttggn attctggaag 120
acttcctaag ctaaaagtat atttacaatat ttacaacaca ngtaaataata acngaagaac 180
tacttcaaatt aangnngaaa ttccagaatt ctanagattt atagctatag ntnacaanta 240
tcaccaattg gtttgcaatc aanngnccag cactacttat gannaangtt taactannaa 300
accaaaaagg gagaaaacct ggnagggaaa nat 333
```

<210> 158

<211> 629

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 345, 565

<223> n = A,T,C or G

<400> 158

```
tcgagcggcc gcccgggcag gtctggtaca tttgtgcgag gtccggcact ctgttctcat 60
ccagtaagtg gtcgagccct ttctgcagaa ttgctgttaa atgttctcct aatagctgtt 120
tctccacaca agcaatcagt ggtttctgtg tgctgtggtc caagtaagtg attactctgt 180
ctccctcttc ttctaagcgt ttacttacat ggtaagata ttctggaacc tctctttcct 240
gcattaacct ttggccttcg gcagcatata agcaattagt ctcttccaaa aatttcagtt 300
caaatgaatc tttatacacc tgcaggtcag acagcatgcc caggaggct ccgcaacagg 360
ctccggtcca cggcctcgcc gtcctctctg cgctcgatca gcagtaggat tccatcaatg 420
gttttactct gaaccatttt atcactaata atatgggttc taaacagttc taatcccata 480
tcccagatgg agggcagcgt ggagttctgc agcacatagg tgcgggtccaa gaacaggaag 540
atgcttctga tcatgaatca tttgnctggc aatggctctg ccagcacgtg gtaatctttc 600
ttttaaaaat aaacccttat ctaaacgtc 629
```

<210> 159

<211> 629

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 33, 546, 576

<223> n = A,T,C or G

<400> 159

```
tcgagcggcc gcccgggcag gttctagagg ganaatctgg ctgatttggg aataaaatat 60
aatcgaatat tcaacacccat gaagataaat cttatttttg aaatctactg accttaatac 120
cccaagcttg ccctgaatac tttgattgga attggaatat atcaaaaaag gttagtattt 180
ttgttgtagt taggatacta aaaggatatt agttacccaa gagatccaat ttgtttttct 240
gatgaatagt gttcagtaaa atgaagcagt cttaaagagt actaataatt tcaaagtgat 300
ttttcgtcta ttcttaatat tttttaatta tttattttta agagttttat accttgagca 360
gatacaatga tccgctttag tgagaggaca atttctgatt gattgttttc tcttcaggcc 420
atctcacctc ttcattctct tgttacattt gaagcagttg atataatggg tttatacttt 480
aaaagataga catggtgccca tgaagtttgg ggaagttggg tgaattatcc cattctagtt 540
acagangagc tttccttaaa tgccttttac ttctangttt ggtcaagaag tcattttctg 600
agtaaaagtt attttcatat atgttgggg 629
```

<210> 160

<211> 519

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 46, 309, 397, 430, 434, 471, 497  
<223> n = A,T,C or G

<400> 160  
tcgagcggcg cgccccgggca ggtctgctgg gattaatgcc aagtntttca gccataaggt 60  
agcgaaatct agcagaatcc agattacatc cacttccaat cagcggtgt ttgggtaatc 120  
cacttagttt ccagataaca tacgtaagaa tgtccactgg gttggaaacc acaattatga 180  
tgcaatcagg actgtacttg acgatctgag gaataatgaa tttgaagaca ttaacatttc 240  
tctgcaccag attgagccga ctctcccctt cttgctgacg gactcctgca gttaccacta 300  
caatcttana attgggcggg tcacagaata atctttatct gccacaattt taggtgctga 360  
agaaataagc tcccatgctg cagatccatc atttctnctt taagottatc ttccaaaaca 420  
tcacacaagan caangttcat cagccagaga ctttcccaga atgctgatag nacacgccat 480  
accaacttgt ccaacancca ctacagcgat cttattggt 519

<210> 161  
<211> 446  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 5, 32, 36, 269, 354, 381  
<223> n = A,T,C or G

<400> 161  
cgagnggccc gcccgggcag gtccagtaag cntttnacga tgatgggaaa ggttatgcaa 60  
ggtcccagcg gtacaacgag ctgtttctac atcatttgta ttctgcatgg tacgtacaat 120  
agcagacacc atctgaggag aacgcatgat agcgtgtctg gaagcttcct ttttagaaag 180  
ctgatggacc ataaactgcag ccttattaac caccacctgg tcctcgatcat ttagcagttt 240  
tgtcagttca gggattgcac gtgtggcang ttctgcatca tcttgatagt taatcaagtt 300  
tacaactggc atgtttcagc atctgcatg ggctcagcaa acgctggaca ttantgggat 360  
gagcagcatc aaactgtgta natgggatct gcattgccctc atctaattgc tcagggaaca 420  
tagcagctcg taccctctga gctcga 446

<210> 162  
<211> 354  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 6, 19, 36, 116, 152, 174, 186, 196, 223, 249  
<223> n = A,T,C or G

<400> 162  
agcgtngtcg cgcccgang tcctgggaag cttttnttgc tgagcctcac agcctctgtc 60  
aggcggctgc ggtaccagcg gtccaccagg ctctcatggc ctccgggctg ggaggngggt 120  
gagggcacaa aacccttccc aaggccacga anggcaaaact tgggtggcatt ccanagcttg 180  
ttgcanaagt ggcgnaacc cagtatccgg ttcacatcca ggntgatgtc acgacctgg 240  
gacatgtang cacataatcc aaaccggaga gcattcgtgc cacattcacg aatccccgct 300  
gggaagtcag ctttctgccc ttctttggcc ttctccacct cgctgggatc cagg 354

<210> 163

<211> 258  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 7, 24, 32, 153, 198, 205  
 <223> n = A,T,C or G

<400> 163  
 tttttcncca agtcctcttg ccgngggatc tngactgcaa ttttaagacac ttctaattag 60  
 ttatacccag gccctgcaaa attgctgggt ttatataata tattcttgct gcacgaagat 120  
 ttattattct gttggatgat tctatttttaa ttntatttat tctggccaaa aaagaacctt 180  
 ctccgctcgt caagagangc caatntgtct tgaaggacaa gagaaagatg ctaacacaca 240  
 ctttcttctt cttgagga 258

<210> 164  
 <211> 282  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 97, 130, 163, 178, 203, 204  
 <223> n = A,T,C or G

<400> 164  
 ggaacatatt acttttaaat tacttgggtc aatgaacat ttaataaaaa catttgcttc 60  
 tctatataat acgtatgtat aaaataagcc ttttcanaaa ctctgggttct cataatcctc 120  
 tataaatcan atgatctgac ttctaagagg aacaaattac agnaaggggt atacattnat 180  
 gaatactggt agtactagag ganngacgct aaaccactct actaccactt gcggaactct 240  
 cacagggtaa atgacaaaagc caatgactga ctctaaaaac aa 282

<210> 165  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 10, 33, 36, 49, 198, 222, 243, 278, 357, 385, 399, 405, 437  
 <223> n = A,T,C or G

<400> 165  
 gcccgggcan gtctctgtaat cccagctact cangangctg agtcatgana atcgcttgaa 60  
 tccgggaggt agaggccgca gcgagcaaa attaagccac tgcaactccag tctgggtgac 120  
 agagttagaa tctgtctgtt gctcctcttg cattgggtctg aaatgggttt gtagaacatg 180  
 ccacagaagg accagcanca gcaacaaatg gatttgtgga angcgtagct ccaaattggag 240  
 cangcacact tgatgaagca cgctgtgtct gtgcagangc aaccactggc actgttccaa 300  
 aaacattgct gctagcatta cttgtggaag tatacgcat actggagggtg gctgcanaac 360  
 tgaaaacgct gtctagttct gccanagctg cataactgnc tgaanatgca cttgactgac 420  
 tgggaactga accacanaac caacaggacc tttacctgtg ga 462

<210> 166  
 <211> 365  
 <212> DNA  
 <213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 14, 18  
<223> n = A,T,C or G

<400> 166  
cgtgggtcgc ggcncgangt ctgaaaccaa tccagaacta aacatcagca cacaaaaaat 60  
accaggatag atggaatcaa aagactctga agccaaaagg aggctaggga gagcaactga 120  
acttagcaag ctgaggactt cagtgtccat catocgatcc tgccctgtaa caacaggctct 180  
atatgataga gatattccat ctgagctgga ggccattatc cttagcaaac taacacagaa 240  
cagaaaacca aatacatgtt ctcatttaga agtaggagct aaatgatgag aactcaagga 300  
cacaaagaaa ggaacaacag acactggggc ctacttgagg gtggagggtg ggaggaggga 360  
gaaga 365

<210> 167  
<211> 364  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 19, 342, 361  
<223> n = A,T,C or G

<400> 167  
agcgtgggtc cggcgcgang tccagcccta gcttgccctg gactccgcct tcaactgggtg 60  
ctctctctaa aagtgtctga ctctttactg tatctcccaa ttccactcc attggttcca 120  
taaggggagg ggtgtctcac tcaacatggt gtccctggta ccaagaactg gctgacgaag 180  
ctgggtgccc tggctcatgc ctgtaatccc agcacttttg ggaggccaag aaggcgcat 240  
cacctgaggt ctggagtcca agatcagcct gaccaacatg atgaaaccaa gtctccacta 300  
aaaatataaa acaattagcc aggcattggt gtgggtgcct gnaatcccag ctactgggga 360  
ngct 364

<210> 168  
<211> 447  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 407, 414, 437  
<223> n = A,T,C or G

<400> 168  
cccgggcagg tcaaaaccca aaacotttca ttttagccca aaccagctca tgattaggta 60  
tacaaggata acagaaccag ttgtcaggac gagcatttga caagtaaaag caattcttgc 120  
aaagctgcag ttcattccagc tcatggcatg tgtctttata tagcatcctc gcaatgtcag 180  
cttgctcact gtctgtctca tagaaaatca cggatttggt gagaagcaat tgggcatcag 240  
ctttgaactc ttcataactt cggatattcc cttcattcac tttctcttga atggtgggaa 300  
cgtccacaga cctcggcgcg gaccacgcta agcccgaatt ctgcagatat ccatcacact 360  
ggcggccgtt cgagcatggc atctagaagg cccaattcgc ctatagnag tcgnattacc 420  
aattcactgg ccgtcgnntt acaacgc 447

<210> 169  
<211> 524  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 4, 6, 39, 40, 235, 248, 313, 340, 359, 382, 389, 420, 434, 442, 453, 496

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 169

```
cgantngcgc gcccgggcag gtctgagcag cttttctggn tgctggacta ttgggattgg 60
gttcatccaa cagagactgt atggatgtta gaatggaaga cacatcatag gttggactcc 120
aacggttctg aagtatgtcc agacatatac taccatctgc atagactaag aacaaagaag 180
taggtacatt aaacgtaaca agaccactaa ggttttaaca ttatagacaa aacanaaata 240
gtcaaganta ctttgctttt gaagtttaaa gattcctatg ttgcttccca gtttaactgcc 300
taaaaagata agncataacc accactagtg aaataatcan gatgatcaga gaatgtcana 360
tgtgatcagt ataaaactgg angatattna gtgtcatcct ttggaaaagg ctgccctatn 420
atccaggaaa tcanaaacat tnttgaacag ggnccctagc tatccacaga catgtgggaa 480
attcattccc caaatngtag gctggatccc ctatctgaaa taac 524
```

&lt;210&gt; 170

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 5, 10, 63, 66, 90, 93, 96, 186, 207, 261, 290, 324, 326

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 170

```
tcgancggcn cgcccgggca ggtgacaaac ctgttattga agatgttggg tctgatgagg 60
aanaanatca gaagggatgg tgacaagaan aanaanaaga agattaagga aaagtacatc 120
gatcaagaag agctcaacaa aacaaagccc atctggacca gaaatcccga cgatattact 180
aatgangagt acggagaatt ctataanagc ttgaccaatg actgggaaga tcacttggca 240
gtgaagcatt tttcagttga nggacagttg gaattcagag cccttctatn tgtcccacga 300
cgtgctcctt ttgatctggt tganancaga aa 332
```

&lt;210&gt; 171

&lt;211&gt; 334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 5, 9, 200, 228, 232

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 171

```
cgagnggcnc gcccgggcag gtctgttgat agcgacttaa cagaaaagtc tagacaaaca 60
taagcataaa aaattacagt ctttctaccc ttgggaatgg ggagaaaaag gaatctctac 120
cccaagacca gaaataataa gtccgttttc tggtcctgaa catccagaat tatggaggct 180
ttggcctgac accacattan aatttgggtc ggaaatcaaa ctttaganac angagatcgt 240
aagccatttt atactatcga cctaaattcc agtctaacgg ttcctttaca aagttgcgga 300
aagccctctt atatgctagc tgtaggaaat atag 334
```

&lt;210&gt; 172

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 19, 375, 388, 390, 395, 409, 426, 434

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 172

```
agcgtggctcg cggcccgang tctgcctata aaactagact tctgacgctg ggctccagct 60
tcattctcac aggtcatcat cctcatccgg gagagcagtt gtctgagcaa cctctaagtc 120
gtgctcatac tgtgctgcc aagctgggtc catgacaact tctgggtggg cgagagcagg 180
catggcaaca aattccaagt tagggctctc aatgagcttc ctgacaagcc agaggaagg 240
cttttcaaag ttgtagttac ttttggcaga aatgtcgtag tactgaagat tcttctttcg 300
gtggaagaca atggatttcg ccttcacttt ctgccttaat atccactttg gtgccacaca 360
acacaatggg gatgntttca cacacttngn accanacttc tatgccagnt aggccatttt 420
ggaagnactt cganggtac                                     439
```

&lt;210&gt; 173

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 5, 31

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 173

```
cgatnggccg cccgggcagg tcctgtaaaa naggaatc agacatcgta cgactcgtaa 60
ttgaatgtgg agctgactgc aatattttgt caaagcacca gaatagtgcc ctgcactttg 120
cgaagcagtc taacaatgtg ottgtgtacg acttgctgaa gaaccattta gagacacttt 180
caagagttagc agaagagaca ataaaggatt actttgaagc tcgccttgct ctgctagaac 240
cagtttttcc aatcgcatgt catcgactct gtgaggggtcc agatttttca acagatttca 300
attaccaacc cccacagaac ataccagaag gctctggcat cctgctggtt atcttccatg 360
caaacttttt gggtaaagaa gttattgctc ggctctgtgg accgtgtagt gtacaagctg 420
tagttctgaa tgataaatct cagcttcctg tttttctggg tctcgtctctg ttgtccaggc 480
tggagtgcag tggcgcggtat tacagctcac tggagtcttg acttccagg cacaagcaat 540
cctccacact cagcctccta actacctggg actaaaaatg caccgccacc acattccgg 599
```

&lt;210&gt; 174

&lt;211&gt; 458

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 30, 32, 35, 51, 61, 213, 261, 327, 347, 359, 377, 418

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 174

```
tcgatttggc cgcccgggca ggtccatgcn gnttntgccc attcccatgg ngcccgacaa 60
ncccatcccc gagggcgaca tcccatgtt catgttcatg cccaccatgc cctggctcat 120
ccctgcgctg ttccccagag gggccattcc catgggtgcc gtcattacac cgggcatgtt 180
cataggcatg ggtcccccca ggagaggggt agnttgaggc cggacaggaa gcatgtttga 240
tggagaactg aggttcacag nctccaaaac tttgagtcac cacattcata ggctgctgca 300
tattctgtct gctgaatcca ttgtatncag tgatggcctg ctggggnttt ggaaggctng 360
cataccaggt agtaagntcg tctagctgta tgtttacacc tggggtcaga ccaagtanga 420
gggcaagggt ttgctgactg attttctgga cccatatc                                     458
```

&lt;210&gt; 175

&lt;211&gt; 1206

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 175

```

ggcacgagga agttttgtgt actgaaaag aaactgtcag aagcaaaaga aataaaatca 60
cagtttagaga accaaaaagt taaatgggaa caagagctct gcagtgtgag gtttctcaca 120
ctcatgaaaa tgaaaattat ctcttacatg aaaattgcat gttgaaaaag gaaattgcc 180
tgctaaaact ggaaatagcc aactgaaac accaatacca ggaaaaggaa aataaatact 240
ttgaggacat taagatttta aaagaaaaga atgctgaact tcagatgacc ctaaaactga 300
aagaggaatc attaaactaaa agggcatctc aatatagtgg gcagcttaaa gttctgatag 360
ctgagaacac aatgctcact tctaaattga aggaaaaaca agacaaagaa atactagagg 420
cagaaattga atcacaccat cctagactgg cttctgctgt acaagaccat gatcaaattg 480
tgacatcaag aaaaagtcaa gaacctgctt tccacattgc aggagatgct tgtttgcaa 540
gaaaaatgaa tgttgatgtg agtagtacga tatataacaa tgagggtgct catcaaccac 600
tttctgaagc tcaaaggaaa tccaaaagcc taaaaattaa tctcaattat gccggagatg 660
ctctaagaga aaatacattg gtttcagaac atgcacaaag agaccaacgt gaaacacagt 720
gtcaaatgaa ggaagctgaa cacatgtatc aaaacgaaca agataatgtg aacaacaca 780
ctgaacagca ggagtctcta gatcagaaat tatttcaact acaaagcaaa aatatgtggc 840
ttcaacagca attagttcat gcacataaga aagctgacaa caaaagcaag ataacaattg 900
atattcattt tcttgagagg aaaatgcaac atcatctcct aaaagagaaa aatgaggaga 960
tatttaatta caataaccat ttaaaaaacc gtatatatca atatgaaaaa gagaaagcag 1020
aaacagaagt tatataatag tataacactg ccaaggagcg gattatctca tcttcacct 1080
gtaattccag tgttgtcac gtggtgttg aataaatgaa taaagaatga gaaaaccaga 1140
agctctgata cataatcata atgataatta ttccaatgca caactacggg tggtgctgct 1200
cgtgcc                                     1206

```

&lt;210&gt; 176

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 176

```

Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn
 1          5          10          15
Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala
 20          25          30
Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys
 35          40          45
Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala
 50          55          60
Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg
 65          70          75          80
Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr
 85          90          95
Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu
100          105          110
Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp
115          120          125
His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His
130          135          140
Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser
145          150          155          160
Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala
165          170          175
Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp
180          185          190
Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln

```

195	200	205
Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn		
210	215	220
Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp		
225	230	235
Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln		
245	250	255
Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile		
260	265	270
Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu		
275	280	285
Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile		
290	295	300
Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Val Ile		
305	310	315

&lt;210&gt; 177

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in the lab

&lt;400&gt; 177

ccaatcatct ccacaggagc

20

&lt;210&gt; 178

&lt;211&gt; 1665

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

```

gcaaaactttc aagcagagcc tcccgcagaag ccactctgcct tcgagcctgc cattgaaatg 60
caaaagtctg ttccaaataa agccttgga ttgaagaatg aacaaacatt gagagcagat 120
cagatgttcc cttcagaatc aaaacaaaag aaggttgaag aaaattcttg ggattctgag 180
agtctccgtg agactgtttc acagaaggat gtgtgtgtac ccaaggctac acatcaaaaa 240
gaaatggata aaataagtgg aaaattagaa gattcaacta gcctatcaaa aatcttggat 300
acagttcatt cttgtgaaag agcaaggga cttcaaaaag atcactgtga acaacgtaca 360
ggaaaaatgg aacaaatgaa aaagaagttt tgtgtactga aaaagaaact gtcagaagca 420
aaagaaataa aatcacagtt agagaaccaa aaagttaaat gggaacaaga gctctgcagt 480
gtgaggtttc tcacactcat gaaaatgaaa attatctctt acatgaaaat tgcattgtga 540
aaaaggaaat tgccatgcta aaactggaaa tagccacact gaaacaccaa taccaggaaa 600
aggaaaataa atactttgag gacattaaga ttttaaaaga aaagaatgct gaacttcaga 660
tgaccctaaa actgaaagag gaatcattaa ctaaaagggc atctcaatat agtgggcagc 720
ttaaagttct gatagctgag aacacaatgc tcacttctaa attgaaggaa aaacaagaca 780
aagaaatact agaggcagaa attgaatcac accatcctag actggcttct gctgtacaag 840
accatgatca aattgtgaca tcaagaaaaa gtcaagaacc tgctttccac attgcaggag 900
atgcttggtt gcaaagaaaa atgaatgttg atgtgagtag tacgatatat aacaatgagg 960
ttgtccatca accactttct gaagctcaaa ggaaatccaa aagcctaaaa attaatctca 1020
attatgccgg agatgctcta agagaaaata cattggtttc agaacatgca caaagagacc 1080
aacgtgaaac acagtgtcaa atgaaggaag ctgaacacat gtatcaaaac gaacaagata 1140
atgtgaacaa acacactgaa cagcaggagt ctctagatca gaaattatct caactacaaa 1200
gcaaaaaatg gtggttcaa cagcaattag ttcattgcaca taagaaagct gacaacaaaa 1260
gcaagataac aattgatatt cattttcttg agaggaat gcaacatcat ctccataaaag 1320
agaaaaatga ggagatattt aattacaata accatttaaa aaaccgtata tatcaatatg 1380
aaaaagagaa agcagaaaca gaaaactcat gagagacaag cagtaagaaa cttcttttgg 1440

```

```

agaacaaca gaccagatct ttactcaca ctcatgctag gaggccagtc ctagcattac 1500
cttatgttga aaatcttacc aatagtctgt gtcaacagaa tacttatttt agaagaaaaa 1560
ttcatgattt cttctgaag cctgggcgac agagcgagac tctgtctcaa aaaaaaaaaa 1620
aaaaaaagaa agaaagaaat gcctgtgctt acttcgcttc ccagg 1665

```

&lt;210&gt; 179

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 179

```

Ala Asn Phe Gln Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro
 1          5          10          15
Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys
 20          25          30
Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser Lys
 35          40          45
Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu
 50          55          60
Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln Lys
 65          70          75          80
Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser
 85          90          95
Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln
100          105          110
Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys
115          120          125
Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys
130          135          140
Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser
145          150          155          160
Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr Met Lys
165          170          175
Ile Ala Cys

```

&lt;210&gt; 180

&lt;211&gt; 1681

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

```

gatacagtca ttcttgtgaa agagcaaggg aacttcaaaa agatcactgt gaacaacgta 60
caggaaaaat ggaacaaatg aaaaagaagt tttgtgtact gaaaaagaaa ctgtcagaag 120
caaaagaaat aaaatcacag tttagagaacc aaaaagttaa atgggaacaa gagctctgca 180
gtgtgagatt gactttaaac caagaagaag agaagagaag aaatgccgat atattaaatg 240
aaaaaattag ggaagaatta ggaagaatcg aagagcagca taggaaagag ttagaagtga 300
aacaacaact tgaacaggct ctccagaatac aagatataga attgaagagt gtagaaagta 360
atattgaatca ggtttctcac actcatgaaa atgaaaatta tctcttacat gaaaattgca 420
tgttgaaaaa ggaaattgcc atgctaaaac tggaaatagc cacactgaaa caccaatacc 480
aggaaaagga aaataaatac tttgaggaca ttaagatttt aaaagaaaag aatgctgaac 540
ttcagatgac cctaaaactg aaagaggaat cattaactaa aagggcacat caatatagt 600
ggcagcttaa agttctgata gctgagaaca caatgctcac ttctaaattg aaggaaaaac 660
aagacaaaga aatactagag gcagaaattg aatcacacca tcctagactg gcttctgctg 720
tacaagacca tgatcaaatt gtgacatcaa gaaaaagtca agaacctgct ttccacattg 780
caggagatgc ttgtttgcaa agaaaaatga atgttgatgt gagtagtacg atatataaca 840
atgaggtgct ccatcaacca ctttctgaag ctcaaaggaa atccaaaagc ctaaaaatta 900

```

```

atctcaatta tgccggagat gctctaagag aaaatacatt ggtttcagaa catgcacaaa 960
gagaccaacg tgaacacacag tgtcaaatga aggaagctga acacatgtat caaacgaac 1020
aagataatgt gaacaaacac actgaacagc aggagtctct agatcagaaa ttatttcaac 1080
tacaagcaaa aaatatgtgg cttcaacagc aattagttca tgcacataag aaagctgaca 1140
acaaaagcaa gataacaatt gatattcatt ttcttgagag gaaaatgcaa catcatctcc 1200
taaaagagaa aaatgaggag atattttaatt acaataacca tttaaaaaac cgtatatatc 1260
aatatgaaaa agagaaagca gaaacagaaa actcatgaga gacaagcagt aagaaacttc 1320
ttttggagaa acaacagacc agatctttac tcacaactca tgctaggagg ccagtcctag 1380
cattacctta tgttgaaaaa tcttaccaat agtctgtgtc aacagaatac ttattttaga 1440
agaaaaattc atgattttctt cctgaagcct acagacataa aataacagtg tgaagaatta 1500
cttggtcacg aattgcataa aagctgccca ggatttccat ctaccctgga tgatgccgga 1560
gacatcattc aatccaacca gaatctcgtc ctgtcactca ggctggagtg cagtgggcgc 1620
aatctcggct cactgcaact ctgcctccca ggttcacgcc attctctggc acagcctccc 1680
g

```

&lt;210&gt; 181

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 181

```

Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys Asp His
1          5          10          15
Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys Lys Phe Cys
20          25          30
Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu
35          40          45
Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu
50          55          60
Thr Leu Asn Gln Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu Asn
65          70          75          80
Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys
85          90          95
Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln Asp
100         105         110
Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His Thr
115         120         125
His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys
130         135         140
Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr
145         150         155         160
Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu
165         170         175
Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu
180         185         190
Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala
195         200         205
Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu
210         215         220
Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala
225         230         235         240
Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro
245         250         255
Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val
260         265         270
Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu
275         280         285
Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr

```

290	295	300
Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln		
305	310	315
Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met		320
	325	330
Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu		335
	340	345
Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu		350
	355	360
Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys		365
	370	375
Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu		380
385	390	395
Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys		400
	405	410
Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser		415
	420	425
		430

&lt;210&gt; 182

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 182

```

gaagtttcat gaggttttagc ttttctgggc tggggagtgg agagaaagaa gttgcagggc 60
ttacaggaaa tcccagagcc tgaggttttc tcccagattt gagaactcta gattctgcat 120
cattatcttt gagtctatat tctcttgggc tgtaagaaga tgaggaatgt aataggctctg 180
ccccaagcct ttcatgcctt ctgtaccaag cttgtttcct tgtgcatcct tcccaggctc 240
tggctgcccc ttattggaga atgtgatttc caagacaatc aatccacaag tgtctaagac 300
tgaatacaaa gaacttcttc aagagttcat agacgacaat gccactacaa atgccataga 360
tgaattgaag gaatgttttc ttaaccaaac ggatgaaact ctgagcaatg ttgaggtgtt 420
tatgcaatta atatatgaca gcagtctttg tgatttattt taactttctg caagaccttt 480
ggctcacaga actgcagggt atggtgagaa a 511

```

&lt;210&gt; 183

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 183

```

cacctcgagg ttcagctcct ctgtcttggg gaagaacctt tcctcggcct ccttgcggtt 60
cttctctgcc atcttctcat actggtcacg catctcgttc agaatgcggc tcaggtccac 120
gccaggtgca gcgtccatct ccacattgac atctccaccc acctggcctc tcagggcatt 180
catctcctcc tcgtggttct tcttcaggta ggccagctcc tccttcaggc tctcaatctg 240
catctccagg tcagctctgg 260

```

&lt;210&gt; 184

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

```

gtctgatggg agaccaaaga atttgcaagt ggatggtttg gtatcactgt aaataaaaag 60
agggcctttt ctactgttat gactgttact tgaccttctt tgaaaagcat tcccaaaatg 120
ctctatttta gatagattaa cattaaccaa cataattttt tttagatcga gtcagcataa 180
atttctaagt cagcctctag tcgtgggttc tctctttcac ctgcatttta tttggtgttt 240
gtctgaagaa aggaaagagg aaagcaaata cgaattgtac tatttgtacc aaatctttgg 300

```

gattcattgg caaataattt cagtgtgggt tattattaaa tagaaaaaaa aaattttggt 360  
 tcctagggtt aaggtctaatt tgataccgtt tgacttatga tgaccattta tgcactttca 420  
 aatgaatttg ctttcaaaat aaatgaagag cagacctcgg c 461

<210> 185

<211> 531

<212> DNA

<213> Homo sapiens

<400> 185

tctgatttta tttccttctc aaaaaaagtt atttacagaa ggtatatatc aacaatctga 60  
 caggcagtga acttgacatg attagctggc atgatttttt cttttttttc ccccaaacat 120  
 tgtttttgtg gccttgaatt ttaagacaaa tattctacac ggcattattgc acaggatgga 180  
 tggcaaaaaa aagtttataa acaaaaaccc ttaacggaac tgcccttaaaa aggcagacgt 240  
 cctagtgcct gtcattgttat attaaacata catacacaca atctttttgc ttattataat 300  
 acagacttaa atgtacaaag atgtttttcca ctttttttcaa ttttttaaca caacagctat 360  
 aaacctgaac acatatgcta tcatcatgcc ataagactaa aacaattata ttttagcgaca 420  
 agtagaaagg attaaatagt caaatacaag aatgaaaaac gcagtacata gtgtcgcgaa 480  
 ctcaaatcgg catttagata gatccagtgg tttaaacggc acgtttttgc t 531

<210> 186

<211> 441

<212> DNA

<213> Homo sapiens

<400> 186

cattcctttc ctgcggttgg gggttctctg tgtcagcgag cctcgggtaca ctgatttcgg 60  
 atcaaaagaa tcatcatctt taccttgact tttcagggaa ttactgaact ttcttctcag 120  
 aagatagggc acagccattg ccttggcctc acttgaaggg tctgcatttg ggtcctctgg 180  
 tctcttgcca agtttcccaa ccaactcgagg gagaaatc gggagggttg acttcctccg 240  
 gggtcttccc gagggcttca ccgtgagccc tgcggccctc agggctgcaa tcctggattc 300  
 aatgtctgaa acctcgctct ctgcctgctg gacttctgag gccgtcactg ccactctgtc 360  
 ctccagctct gacagctcct catctgtggt cctgttgtac tggacgggggt cccaggggtc 420  
 ctgggggctt ttttctgtc t 441

<210> 187

<211> 371

<212> DNA

<213> Homo sapiens

<400> 187

aaaagtgaat gagtaactat tatattgttg gcaataataa gttgcaaaat catcaggctg 60  
 caggctgctg atgggtgagag tgaactctgt cccagatcca ctgccgctga accttgatgg 120  
 gacccagat tctaaactag acgccttatg gatcaggagc tttggggctt tccctgggtt 180  
 ctgttgatac caggccaacc aactactaac actctgactg gcccggaag tgatggtgac 240  
 tctgtctcct acagttgcag acagggtgga aggagactgg gtcactctga tgtcacattt 300  
 ggcacctggg agccagagca gcaggagccc caggagctga gcggggaccc tcatgtccat 360  
 gctgagtcct g 371

<210> 188

<211> 226

<212> DNA

<213> Homo sapiens

<400> 188

ggtatataaa ttgagatgcc cccccaggcc agcaaatgtt cctttttgtt caaagtctat 60  
 ttttattcct tgatattttt cttttttttt tttttgtgga tggggacttg tgaatttttc 120  
 taaagggtct atttaacatg ggaggagagc gtgtgcggct ccagcccagc ccgctgctca 180

ctttccaccc tctctccacc tgcctctggc ttctcaggac ctgcc

226

<210> 189

<211> 391

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 43, 112, 131, 156, 195, 208, 221, 317, 333, 367

<223> n = A,T,C or G

<400> 189

tggtggaagt ttattctgtt ttcacatcta ggttggtggg ganagtgata gacaaagttc 60  
 tggattctgg gcatcgctcg cgcgtgcttg taatcctact tgggaggttg anacaggaga 120  
 cctcgccgcg naccacgcta agggcgaatt ctgcanatat ccatcacact ggcggccgct 180  
 cgagcatgca tctanagggc ocaattcncc ctatagttag ncgtattaca attcactggc 240  
 cgctgcttta caacgtcgtg actgggaaaa ccttgccgtt acccaactta atcgcccttg 300  
 agcacatccc cctttcncca gctggcttaa tancgaagag gcccgccaccg atcgcccttc 360  
 ccaacanttg cgcagcctga atggcgaatg g 391

<210> 190

<211> 501

<212> DNA

<213> Homo sapiens

<400> 190

catcttgccc tttttgagct gtttccgctt cttctcatcc cggtcactgt caccctcatt 60  
 actggaggag ctggcagagg cggttgctgtc aaactcctct gccacatctt cctcctcttc 120  
 acctggggtg aatgactcat cggtttcttc tctgagtca tcgctgctgt cattggcatt 180  
 ctccctcccg atcttgccct cctccttcat cctctccaag taggcatcat gctggtcctc 240  
 atcagagtca gcatattcat cgtagcttgg gttcatgccc tctttcaatc ctcggttttt 300  
 gatggttgagc tttttcgcgt tgacaaaatc aaacagtttc ccgtactcct ccctctcaat 360  
 gctgctgaag gtatactgag tgccctgctt ggtctcaatt tcaaagtcaa aggaacgagt 420  
 agtagtggtg ccacgagcaa agttgacaaa ggagatctca tcgaagcgga tgtgcacagg 480  
 tggcttggtg acgtagatga a 501

<210> 191

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 49

<223> n = A,T,C or G

<400> 191

ggaaaaactg tgaaaaatat atctgaatth attaatgaca gtataaaaana gggttgtggc 60  
 aacagaaaagt aaaaactaac atggattgct ataaatatgc tgaagcctag ttgttcaaat 120  
 gatacaattc tctcatgcta ctctaaagtt tataaagaaa aaggatttac actttacaca 180  
 ctgtacacaa aaggaatacc ttctgagagc cagggagtgg ggaaagggga aggagacttg 240  
 a 241

<210> 192

<211> 271

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 6, 17, 23, 26, 70, 227, 245

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 192

```
tggtcntgga ttacacanata aantanatcg actaaaactg gcagaaattg tgaagcaggt 60
gatagaagan caaaccacgt cccacgaatc ccaataatga cagcttcaga ctttgctttt 120
ttaacaattt gaaaaattat tctttaatgt ataaagtaat tttatgtaa ttaataaatc 180
ataatttcat ttccacattg attaaagctg ctgtatagat ttaggngnca ggacttaata 240
atagnngaaa tgaaattatg atttattaat c                               271
```

&lt;210&gt; 193

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 193

```
agtcgaggcg ctgatcccta aaatggcgaa catgtgtttt catcatttca gccaaagtcc 60
taacttccct tgcccttccct atcacctcga gaagtaatta tcagttgggt tggatttttg 120
gaccaccgtt cagtcatttt gggttgccgt gctcccaaaa cattttaaat gaaagtattg 180
gcattcaaaa agacagcaga caaaatgaaa gaaaatgaga gcagaaagta agcatttcca 240
gcctatctaa tttctttagt tttctatttg cctccagtgc agtccatttc ctaatgtata 300
ccagcctact gtactattta aaatgctcaa tttcagcacc gatggacctg c           351
```

&lt;210&gt; 194

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

```
ctgagacaca gaggccact gcgaggggga cagtggcggt gggactgacc tgctgacagt 60
caccctccct ctgctgggat gaggtccagg agccaactaa aacaatggca gaggagacat 120
ctctggtgtt cccaccaccc tagatgaaaa tccacagcac agacctctac cgtgtttctc 180
ttccatccct aaaccacttc cttaaaatgt ttggatttgc aaagccaatt tggggcctgt 240
ggagccctgg gttggatagg gccatggctg gtcccccacc atacctcccc tccacatcac 300
tgacacagac c                               311
```

&lt;210&gt; 195

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```
tgtcagagtg gcactggtag aagttccagg aaccctgaac tgtaagggtt cttcatcagt 60
gccaacagga tgacatgaaa tgatgtactc agaagtgtcc tggaatggg cccatgagat 120
ggttgtctga gagagagctt cttgtcctgt ctttttcctt ccaatcaggg gctcgtctt 180
ctgattattc ttcagggcaa tgacataaat tgtatattcg gttcccggtt ccaggccagt 240
aatagtagcc tctgtgacac cagggcgggg ccgagggacc acttctctgg gaggagaccc 300
aggcttctca tacttgatga tgtagccggt aatcctggca cgtggcggtt gccatgatac 360
cagcagggaa ttgggtgtgg t                               381
```

&lt;210&gt; 196

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

```
cacaaacaag aggagcacca gacctcctct tggtctcgag atggcttcgc cacaccaaga 60
gcccaaacct ggagacctga ttgagatttt ccgccttgcc tatgagcaact gggccctgta 120
tataggagat ggctacgtga tccatctggc tcctccaagt gactaccccg gggctggctc 180
ctccagtgtc ttctcagtc tgagcaacag tgcagaggtg aaacgggagc gcctggaaga 240
tgtgtgtggga ggctgttgct atcgggtcaa caacagcttg gacctgagt accaaccacg 300
gcccgtaggag gtgatcacca gttctgcgaa ggagatggtt ggtcagaaga tgaagtacag 360
tattgtgagc aggaactgtg agcactttgt caccagacc t 401
```

&lt;210&gt; 197

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 197

```
ctgtaatgat gtgagcagg agccttcctc cctggggccac ctgcagagag ctttcccacc 60
aactttgtac cttgattgcc ttacaaagt atttgtttac aaacagcgac catataaaag 120
cctcctgccc caaagcttgt gggcacatgg gcacatacag actcacatac agacacacac 180
atatatgtac agacatgtac totcacacac acaggcacca gcatacacac gtttttctag 240
gtacagctcc caggaacagc taggtgggaa agtcccatca ctgagggagc ctaaccatgt 300
ccctgaacaa aaattgggca ctcatctatt ctttttctct tegtcccta ctattgaaa 360
ccaaactctg gaaaggacc aatgtaccag tatttatacc tctagtgaag cacagagaga 420
ggaagagagc tgcttaaaact cacacaacaa tgaactgcag acacagacct g 471
```

&lt;210&gt; 198

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 198

```
ggtccattga ggctctgtcg gccatgcccc cagttcgaag ctttgccaac gaggaggcg 60
aagcccagaa gtttagggaa aagctgcaag aaataaagac actcaaccag aaggaggctg 120
tgccctatgc agtcaactcc tggaccacta gtatttcagg tatgtgctg aaagtgggaa 180
tcctctacat tgggtgggag a 201
```

&lt;210&gt; 199

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 199

```
tctggcacag atcttcaccc acacggcggc ccacgtgctg atcatcttcc ggggtctcacc 60
gggcctggaa cacaccatct tcccctatgag ccggtgccc agtctggtga cttccatctt 120
ggcccctggc cttatgtccc agttatgacc cctgacttca actctggctc ttaccctgta 180
actccagtcc atctctgaca tttttaacac ccggccttgt gaccgtggac atagctcctg 240
acctcgattc catctttgag cccagtgtta gtccatgaga tcatgacctg actcctggctc 300
tccaaccttg tgatcctaata tctgggacct caatcctagc ctctgaactt gggaccctgg 360
agctcctgac cttagtcttg accgctaccc ttgattctga cctttgatcc tgtaacttag 420
gggtggcccc tgaccttatt actgtcattt agtccttga ccttgccact tcaatcctgg 480
ctttatgacc tcctactctc aattttaact ttaaccaaata gaccaaattt gtgacactaa 540
atgaccacaa t 551
```

&lt;210&gt; 200

&lt;211&gt; 211

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature

<222> 8, 36, 40, 78, 165, 170, 171, 173, 203, 207, 208

<223> n = A,T,C or G

<400> 200

```
cagctcancg ggcgacatgc ccctacaagt tggcanaagn ggctgccact gctggggtttg 60
tgtaagagag gctgctgnca ccattacctg cagaaacctt ctcatagggg ctacgatcgg 120
tactgctagg gggcacatag cgcccatggg tgtggtaggt ggggnactcn ntnataggat 180
ggtaggatc ccgggctgga aanatgnnca g 211
```

<210> 201

<211> 111

<212> DNA

<213> Homo sapiens

<400> 201

```
ccagtgaag gaaacaaaac tggcagtttg tccatttgaa tatcagacct agtttcttct 60
taatttccac actatttctc ccatattcct taaacttctt ggcatccacc t 111
```

<210> 202

<211> 331

<212> DNA

<213> Homo sapiens

<400> 202

```
tgaaaataca gaataccagg tgggtccaaa tgtttgaagt tctttgaaca gaaagagaga 60
ggagagagag agagaggaaa attccctaac ccttggttta aagacaatat tcattttattg 120
ctcaaagtat gcttttaagg gaggacagtg gaataaaata aacttttttt ttctccctac 180
aatacataga agggttatca aaccactcaa gtttcaaaat ctttccaggg tccaatatca 240
ctttttttct ttcggttcaa tgaaaagcta aatgtaataa tactaattat agataaaatt 300
ttattttact ttttaaaaat ttgtccagac c 331
```

<210> 203

<211> 491

<212> DNA

<213> Homo sapiens

<400> 203

```
agtcaaccag tctacttagt acctggttgc tgcctctgac cttttcagct tgataccctg 60
ggcttttagt taaccaataa atctgtagtg accttacctg tattccctgt gctatccctg 120
gggaaggtag gaatgggcta agtatgatga atgtataggt tagggatctt ttgggtttta 180
atcacagaaa acctaatcca aactggctta aaataaaaag gattttattg ttcattgtaac 240
tagaaagtcc ataggtagtg ctggctccag gtgaagactt gacctcagtag ttcagtatgt 300
ctctaaatac cggactgact tttttctcac tgttgcatct tctgtaggac catttaagtc 360
tgggccactt aatggctgcc agcattccta agattacact tttcccccatt tatgtccaat 420
cagaaaaaga aggcattctt gtaccagaaa tctcagcaaa agccctaata ttcacactga 480
ttaggacctg c 491
```

<210> 204

<211> 361

<212> DNA

<213> Homo sapiens

<400> 204

```
tcctttcttc ccccatgtga taaatgggtc cagggctgat caaagaactc tgactgcaga 60
actgccgctc tcagtggaca gggcatctgt taccctgaga cctgtggcag acacgtcttg 120
ttttcatttg atttttgtta agagtgcagt attgcagagt ctagaggaat ttttgtttcc 180
ttgattaaca tgattttcct ggttgttaca tccagggcat ggcagtggcc tcagccttaa 240
```

acttttgttc ctactccac cctcagcgaa ctgggcagca cggggagggg ttggctaccc 300  
ctgcccattc ctgagccagg taccaccatt gtaaggaaac actttcagaa attcagacct 360  
c 361

<210> 205

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 2, 3

<223> n = A,T,C or G

<400> 205

cnngtacagt tcttcctgga tggccgacac agatcctggg gaaaggcaat cctggcactg 60  
ctctgaaacc agagctcctc ctccctcccc gggcaggggt gagctgagaa gggctgctct 120  
agcgttgagg ctccacctcc atacacctga tatcttgata gggcaggtcc ctgctatggg 180  
ccactgttct gggcagtata gtatgcttga cagcatcctt ggcattctat caccagatcc 240  
cagagcaccg gctactagct gtgacaacat cctccaaaca ttgcaaaatt tcccctggga 300  
ggcaagattg cctcagatgg gagaatcacg ctctagggaa atctgctggt atgagaaccc 360  
caactcccca ctccactgag cctccagatg gcgagcaggc tgcagctcca gcacagacac 420  
gaagctccct ccagccactg acgggtccatg gctgggggta cccaggacct c 471

<210> 206

<211> 261

<212> DNA

<213> Homo sapiens

<400> 206

tagagtattt agagtcttga gataacaagg aatccaggca tccttttagac agtcttctgt 60  
tgtcctttct tcccaatcag agatttgtgg atgtgtggaa tgacaccacc accagcaatt 120  
gtagccttga tgagagaatc caattcttca tctccacgaa tagcaagttg caagtgcaga 180  
ggggtaatac gctttacctt taagtctttt gatgcatttc ctgccagttc aagtacctct 240  
gcgggtgaggt actccaggat g 261

<210> 207

<211> 361

<212> DNA

<213> Homo sapiens

<400> 207

gctctccggg agcttgaaga agaaactggc tacaaagggg acattgccga atgttctcca 60  
gcggctctgta tggaccaggg cttgtcaaac tgtactatac acatcgtgac agtcaccatt 120  
aacggagatg atgccgaaaa cgcaaggccg aagccaaagc caggggatgg agagtttgtg 180  
gaagtcattt ctttacccaa gaatgacctg ctgcagagac ttgatgctct ggtagctgaa 240  
gaacatctca cagtggacgc caggggtctat tcctacgctc tagcactgaa acatgcaaat 300  
gcaaagccat ttgaagtgc cttcttgaaa ttttaagccc aaatatgaca ctggacctgc 360  
c 361

<210> 208

<211> 381

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 10, 27, 37, 46, 75, 95, 102, 137, 143, 202, 234, 278, 310,

351

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 208

```

agaggagatn tttgccatgc ctgaatnctt tcctatncca ccctancact taacatatta 60
cttagtctgc tttgntaaaa gcaagtatta ccttnaactt gncctctact ctttgccctt 120
tagctaacta ataaagnttg atntaggcat tattatataa ttctgagtc ttcattggtat 180
ctctcatggt tgatgtatgt tncaaaactaa gatctatgat agtttttttt ccanagtctc 240
attaaatcat ttatttcctt tactttctca cctctgtnga aacattttaga aactggattt 300
gggaacccan ttttgaaaaa ccagattcat agtcatgaaa atggaaactt ncatattctg 360
tttttgaaaa gatgtggacc t 381

```

&lt;210&gt; 209

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 83

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 209

```

gtggagagca agtgatttat taaagcaaga cgttgaaacc tttacattct gcagtgaaga 60
tcagggtgtc attgaaagac agnggaaacc aggatgaaag tttttacatg tcacacacta 120
catttcttca atattttcac caggacttcc gcaatgaggc ttctgtttctg aaggacacac 180
tgatccgtgc atctcttcac tcctaacttg gctgcaacag cttccacctg c 231

```

&lt;210&gt; 210

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 210

```

tccatcctgg ttttgcagag atcaggttgt tgacagttcc tgggtgacct acagctacct 60
atgtcagtta tctccactaa catatccaag aatctttgta ggacaatttc tccacctgca 120
aggtttttta ggtagaactc ttcttttaag gcaattagcc cattgccaaa aggttttact 180
gtcttaaaagc tgtctttctg agatctaatt ccaaggactt ctccacagct aagtgaagatg 240
cctcacacca ttaggtgatg ctttggacag aacagagtat tttcatcttg tgtttaaagc 300
aatcctctgg cttcggtctc tcaccacttt ctatgccagt ctcccattta tgtccctagt 360
aatgcctatg c 371

```

&lt;210&gt; 211

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 211

```

tttatittta aagaaaaaaa ttaaaataga gccaacaaat gcaattaaga aaaaaaagt 60
attgagacac aaggggacct acatgttctg gtctaagaag catgcaagta ttacaaagca 120
ttccagatac agtatgacag aggaacagtg aacaagcatt ggaacgatgc tctttcttct 180
agaacaggga agtctaacag ttatgttttc acaatggtag tgattaaacc atctttatct 240
ttaagggaatt ttatagggaag aattttagca ccatcattaa aggaaaaata ataatacctt 300
tttagccctg cctatctcca gtottggaat aataacagaa gcatagcaac tttcagatc 360
taaaatataa acaagaatag taagtccatc ccagcttcta gagatgaggt agctcatgct 420
aagaaatgtt ggggtcatttt tcctatgaaa gttcaaaggc caaatggtca c 471

```

&lt;210&gt; 212

<211> 401  
<212> DNA  
<213> Homo sapiens

<400> 212  
tggcctgtct ccttcacata gtccatatca ccacaaatca cacaacaaaa gggagaggat 60  
atattttggg ttcaaaaaaa gtaaaaagat aatgtagctg catttctttg gttatttttg 120  
gccccaaata tttcctcatc tttttgttgt tgctatggat ggtggtgaca tggacttgtt 180  
tatagaggac aggtcagctc totggctcgg tgatctacat tctgaagtgg tctgaaaatg 240  
tcttcatgat taaattcagc ctaaactgtt tgccgggaac actgcagaga caatgctgtg 300  
agtttccaac ctcagcccat ctgcgggcag agaaggtcta gtttgtccat caccattatg 360  
atatcaggac tggttacttg gttaaggagg ggtctacctc g 401

<210> 213  
<211> 461  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 239, 290, 358, 359, 391, 393  
<223> n = A,T,C or G

<400> 213  
tgtgaagcat acataaataa atgaagtaag ccatactgat ttaatttatt ggatgttatt 60  
ttccctaaga cctgaaaatg aacatagtagt gctagtattt ttccagtgtt agccttttac 120  
tttcctcaca caatttggaa tcatataata taggtacttt gtccctgatt aaataatgtg 180  
acggatagaa tgcatacaagt gtttattatg aaaagagtgg aaaagtatat agcttttanc 240  
aaaaggtggt tgcccattct aagaaatgag cgaatatata gaaatagtgn gggcatttct 300  
tcctgttagg tggagtgtat gtgttgacat ttctcccat ctctcccat tctgtttnt 360  
ccccattatt tgaataaagt gactgctgaa nangactttg aatccttacc cacttaattt 420  
aatgtttaa gaaaaaccta taatggaaa gtagactcct t 461

<210> 214  
<211> 181  
<212> DNA  
<213> Homo sapiens

<400> 214  
cctgagcttc tactccttcc ccttaagatt cctccaaagc accagctcca taaaatcctt 60  
cagctcccca gaccacacc aagaaccca catgttaatt ggatcagcca aatctacaag 120  
cagataagtc ctaaggagaa tgccgaagcg tttttcttct tcctcaagcc tagcatgaga 180  
c 181

<210> 215  
<211> 581  
<212> DNA  
<213> Homo sapiens

<400> 215  
ctgctttaag aatggttttc caccttttcc ccctaattct taccaatcag acacatttta 60  
ttattttaaat ctgcacctct ctctatttta ttggccaggg gcacgatgtg acatatctgc 120  
agtcccagca cagtgggaca aaaagaattt agaccccaaa agtgcctctg gcatggatct 180  
tgaacagAAC cagtatctgt catggaactg aacattcatc gatggctctc atgtattcat 240  
ttattcactt gttcattcaa gtatttattg aatacctgcc tcaagctaga gagaaaagag 300  
agtgcgcttt ggaaatttat tccagttttc agcctacagc agattatcag ctccggtgact 360  
tttctttctg ccaccattta ggtgatgtg tttgattcag agatggctga atttctattc 420  
ttagcttatt gtgactgttt cagatctagt ttgggaacag attagaggcc attgtcctct 480

gtcctgatca ggtggcctgg ctgtttcttt ggatccctct gtcccagagc caccagaaac 540  
cctgactctt gagaatcaag aaaaacacca gaaaggacct c 581

<210> 216

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 37, 38, 164, 176, 254

<223> n = A,T,C or G

<400> 216

ccgatgtcct gcttctgttg accaggggct cctctgnngg tggcctcaac cacggctgag 60  
atccctagaa gtccaggagc tgtggggaag agaagcactt agggccagcc agccgggcac 120  
ccccacttgc gccccgaccc acgctcacgc accagacctg cccnggcggg cgctcnaaag 180  
ggcgaattct gcagatatcc atcacactgg cggacgctcg agcatgcac tagagggccc 240  
aattcacctt atantgagtc gtattacaat tcaactggccg t 281

<210> 217

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 33, 322

<223> n = A,T,C or G

<400> 217

atagcagggt tcaacaattg tctttagatt tgnagtaaaa agacataaga aagagaagggt 60  
gtggtttgca gcaatccgta gttggtttct caccataccc tgcagttctg tgagccaaag 120  
gtcttcgaga aagttaaaat aaatcacaaa gactgctgtc atatattaat tgcataaaca 180  
cctcaacatt gctcagagtt tcatccgttt ggtaagaaa acattccttc aattcatcta 240  
tggcatttgt agtggcattg tctgttatga actottgaag aagttctttg tattcagtct 300  
tagacacttg tggattgatt gncctggaaa tcacattctc caataaggga cctcgg 356

<210> 218

<211> 321

<212> DNA

<213> Homo sapiens

<400> 218

ttgtccatcg ggagaaagggt gtttgtcagt tgtttcataa accagattga ggaggacaaa 60  
ctgctctgcc aatttctgga tttctttatt ttcagcaaac actttcttta aagcttgact 120  
gtgtgggcac tcatccaagt gatgaataat catcaagggt ttgttgcttg tcttgatttt 180  
atatagagct tcttcatatg tctgagtcca gatgagttgg tcacccaac ctctggagag 240  
ggtctggggc agtttgggtc gagagtcctt tgtgtccttt ttggtccag gtttgactgt 300  
ggtatctctg gacctgcctg g 321

<210> 219

<211> 271

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 41

<223> n = A,T,C or G

<400> 219

```
ccggttaggt ccacgcgggg gcagtggagg cacaggctca nggtggccgg gctacctggc 60
accctatggc ttacaaagta gaggtagggc agtttccttc cacctgaggg gagcactctg 120
actcctaaca gtcttccttg ccctgccatc atctgggggtg gctggctgtc aagaaaggcc 180
gggcatgctt tctaaacaca gccacaggag gcttgtaggg catcttcag gtggggaaac 240
agtcttagat aagtaagggtg acttgtctaa g 271
```

<210> 220

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 32, 43

<223> n = A,T,C or G

<400> 220

```
gtcctacgac gaggaccagc tttcttctt cnacttttcc canaactctc ggggtgcctcg 60
cctgcccgaa tttgctgact gggctcagga acaggagat gctcctgcc ttttatttga 120
caaagagttc tgcgagtggg tgatccagca aatagggcc aaacttgatg ggaaaatccc 180
ggtgtccaga gggtttctta tcgctgaagt gtacacgctg aagccccctg agtttgcaa 240
gcccaacact ttggtctgtt ttgtcagtaa tctcttccca cccatgctga cagtgaactg 300
gtagcatcat tccgtccctg tgggaaggatt tgggcctact tttgtctcag a 351
```

<210> 221

<211> 371

<212> DNA

<213> Homo sapiens

<400> 221

```
gtctgcagaa gcgtgtctga ggtgtccggt ggaggtggca gccgagctct gggactaatc 60
accgtgctgg ggacggcacc gcgtcaggat gcaggcagat ccctgcagaa gtgtctaaaa 120
ttcacactcc tcttctggag ggacgtcgat ggtattagga tagaagcacc aggggacccc 180
acgaacggtg tcgtcgaaac agcagccctt atttgcacac tgggaggggc tgacaccagg 240
aaaaccacaa ttctgtcttt cacggggggc cactgtacac gtctctgtct gggcctcggc 300
cagggtgccg agggccagca tggacaccag gaccagggcg cagatcacct tgttctccat 360
ggtggacctc g 371
```

<210> 222

<211> 471

<212> DNA

<213> Homo sapiens

<400> 222

```
gtccatgttc catcattaat gttccaacat caccagggac acaaagctgc aaaaatgaga 60
agggaaataa ggttagagaa aggatccggg caatcttaag gactgaggaa gacatgttcc 120
ccaacccttg aactcacaaa ccctgaagct caaggattgc atccttcctc caaatctcac 180
tcaacataat aagtgcagaa caacatgcc aagcactgta tgaagcacta gggacaaaaga 240
caaggtcaaa atccttgtaa ccaaatttaa tggattgta atgcagtgtt aacacaggac 300
agtaacagaa caccacagaa gagggtaggg ataagcataa atgaagtaac 360
atgaataaaa cttccaaatg gaaaacttgt ccataccccc agggcaagtc aactacagtc 420
tcccaaagga cataaattcc acttagggca cactagacag aaaacaatat t 471
```

<210> 223

<211> 411  
 <212> DNA  
 <213> Homo sapiens

<400> 223  
 agttgctcta caatgacaca caaatcccg taaataaatt ataaacaagg gtcaattcaa 60  
 atttgaagta atgttttagt aaggagagat tagaagacaa caggcatagc aaatgacata 120  
 agctaccgat taactaatcg gaacatgtaa aacagttaca aaaataaacg aactctcctc 180  
 ttgtcctaca atgaaagccc tcatgtgcag tagagatgca gtttcatcaa agaacaaca 240  
 tccttgcaaa tgggtgtgac gcggttccag atgtggattt ggcaaacct catttaagta 300  
 aaaggtttagc agagcaaagt gcggtgcttt agctgctgct tgtgccgctg tggcgtcggg 360  
 gaggtcctcg cctgagcttc cttccccagc tttgctgcct gagaggaacc a 411

<210> 224  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 31  
 <223> n = A,T,C or G

<400> 224  
 ggtctgaagt ttgataacaa agaaatatat ntaagacaaa aatagacaag agttaacaat 60  
 aaaaacacaa ctatctgttg acataacata tggaaacttt ttgtcagaaa gctacatctt 120  
 cttaatctga ttgtccaaat cattaataa tggatgattc agtgccattt tgccagaaat 180  
 tcgtttggct ggatcataga ttaacatttt cgagagcaaa tccaagccat tttcatccaa 240  
 gtttttgaca tgggatgcta ggcttcctgg tttccatttg ggaaatgtat tcttatagtc 300  
 ctgtaaagat tccacttctg g 321

<210> 225  
 <211> 251  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 34  
 <223> n = A,T,C or G

<400> 225  
 atgtctgggg aaagagttca ttggcaaaag tgtnotccca agaatggttt acaccaagca 60  
 gagaggacat gtcactgaat ggggaaaggg aacccccgta tccacagtca ctgtaagcat 120  
 ccagtaggca ggaagatggc tttgggcagt ggctggatga aagcagattt gagataccca 180  
 gctccggaac gaggtcatct tctacaggtt cttccttcac tgagacaatg aattcagggt 240  
 gatcattctc t 251

<210> 226  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 26, 34, 35, 36, 37, 39  
 <223> n = A,T,C or G

&lt;400&gt; 226

```
gttaggtccc agggcccccg ccaagnggtt accnnnnntna ccactcctga cccaaaaatc 60
aggcatggca ttaaaacgtt gcaaattcct ttactgttat cccccccacc accaggacca 120
tgtaggggtgc agtctttact ccctaaccg tttcccga aaaggtgctac ctcctttcca 180
gacagatgag agagggcagg acttcaggct ggatccacca ctgggctctc cctccccag 240
cctggagcac gggaggggag gtgacggctg gtgactgatg gatgggtagt gggctgagaa 300
gaggggacta ggaagggcta ttccaggctc a                                     331
```

&lt;210&gt; 227

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

```
aggtctgccc ttgaagtata ggaaggaatc atagtggag gacttctgca ttatttgttg 60
gctgaagcta gaagtgaac cccctcctga tttctgcagc aagatgaact gccttatccc 120
cagcccgcag gaatgttcat atctgagcaa tcaatgggca ctgtgttcaa ccacgccatt 180
ttcaagattg gctccttaaa ccaccacaaa ggcaccagct ctgggagaag ctgcaggagg 240
aagagaacaa agccctcgct gtgatcagga tgggtgtctc ataccttttc tctgggggtca 300
ttccaggtat gagacagagt tgaacctgcg catgagcgtg gaggccgaca tcaacggcct 360
gcgcaggggtg ctggatgagc tgaccctgga c                                     391
```

&lt;210&gt; 228

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 35

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 228

```
gttgtccata gccacctcct gggatagaag cttntagtt catagttcga ttagtggtgc 60
cttaggacat aggtccagcc ctacagatta gctgggtgaa gaaggcaagt gtctcgacag 120
ggcttagtct ccacctcag gcatggaacc attcagggtg aagcctggga tgtgggcaca 180
ggagactcag gctgatataa aaataacaaa atcagtaata aaaaaattat aaaacctgtt 240
gcttgtctga atagatttga gcaacagtct tgcctttgtt aaaatcctgg agccgttaag 300
tcctgaatat tcttctggac atcattgctg gctggagaaa ggagccccag gcccggtcgc 360
gctgacatct gtcaggtttg gaagtctcat c                                     391
```

&lt;210&gt; 229

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 202

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 229

```
gtccatggct tctcaccag acagtcttct tgggcaactt ggggaagccc ctgttctgct 60
caagtctcac cccatggaag aggtggggga agggggcctt ggtttttcag gaagacgggt 120
tgagagcac gagtcactac aaagcagtaa aagtgaatgg tgtctccagg ggctgggtcc 180
agaacaccgc ggagagcccc anccataaag gtgtgttccg cctctggcct gcaggaatct 240
ctttgaatct ctttgattgg tggctccaag agcaatggga agtcaacagc caggaggctg 300
gactgggttc cctgggacct cgaggtccca gaggtgctg g                                     341
```

<210> 230  
<211> 511  
<212> DNA  
<213> Homo sapiens

<400> 230  
gtccaagcca aggaaacccat tcccttacag gagacctccc tgtacacaca ggaccgcctg 60  
gggctaaagg aaatggacaa tgcaggacag ctagtgtttc tggctacaga aggggacctat 120  
cttcagttgt ctgaagaatg gttttatgcc cacatcatac cattccttgg atgaaacccg 180  
tatagttcac aatagagctc agggagcccc taactcttcc aaaccacatg ggagacagtt 240  
tccttcatgc ccaagcctga gctcagatcc agcttgcaac taatccttct atcatctaac 300  
atgccctact tggaaagatc taagatctga atcttatcct ttgccatctt ctgttacctat 360  
atggtgttga atgcaagttt aattaccatg gagattgttt tacaaaacttt tgatgtggtc 420  
aagttcagtt ttagaaaagg gagtctgttc cagatcagtg ccagaactgt gcccaggccc 480  
aaaggagaca actaactaaa gtagtgagat a 511

<210> 231  
<211> 311  
<212> DNA  
<213> Homo sapiens

<400> 231  
ggtccaagta agctgtgggc aggcaagccc ttcggtcacc tgttggttac acagaccctt 60  
cccctcgtgt cagctcaggc agctcgaggc ccccgaccaa cacttgacag ggtccctgct 120  
agttagcgcc ccaccgccgt ggagttogta ccgcttcctt agaacttcta cagaagccaa 180  
gctccctgga gccctgttgg cagctctagc tttgcagtcg tgtaattggc ccaagtcatt 240  
gtttttctcg cctcactttc caccaagtggt cttagagtcac gtgagcctcg tgtcatctcc 300  
ggggtggacc t 311

<210> 232  
<211> 351  
<212> DNA  
<213> Homo sapiens

<400> 232  
tcgttttagct aataatccct tccttgatga tacactccaa cttcttggtt ttctttatct 60  
ctaaaaagcg gttctgtaac totcaatcca gagatgttaa aaatgtttct aggcacggta 120  
ttagtaaatc aagtaaatct catgtcctct taaaggacaa acttcagag atttgaatat 180  
aaatttttat atgtgttatt gattgtcgtg taacaaatgg cccccacaaa ttagtagctt 240  
aaaatagcat ttatgatgtc actgttttct ttgccttttc attaatgttc tgtacagacc 300  
tatgtaaaaca acttttgtat atgcatatag gatagctttt ttgaggggtat a 351

<210> 233  
<211> 511  
<212> DNA  
<213> Homo sapiens

<400> 233  
aggctctggat gtaaggatgg atgctctcta tacatgctgg gttggggatg ctgggactgc 60  
acagccacccc ccagtatgcc gctccaggac tctgggacta gggcgccaaa gtgtgcaaat 120  
gaaaatacag gataccacag gaactttgaa tttcagattg tgaaaagaaa acaaatcttg 180  
agactccaca atcaccaagc taaaggaaaa agtcaagctg ggaactgctt agggcacaagc 240  
tgccctcccat tctattcaca gtcacccccc tgaggctcac ctgcatagct gattgcttcc 300  
tttcccctat cgcttctgta aaaatgcaga ctactgagc cagactaaat tgtgtgttca 360  
gtggaaggct gatcaagaac tcaaaagaat gcaacctttt gtctcttata tactacaacc 420  
aggaagcccc cacttaaggg ttgtcccacc ttaactggact gaaccaaggt acatcttaca 480  
cctactgatt gatgtctcat gtccccctaa g 511

<210> 234  
<211> 221  
<212> DNA  
<213> Homo sapiens

<400> 234  
caggctccagc gaaggggctt cataggctac accaagcatg tccacataac cgaggaagct 60  
ctctccatca gcatagcctc cgatgaccat ggtgttccac aaaggggtca tcttcgagcg 120  
ccggctgtac atggccctgg tcagccatga atgaatagct ctaggactat agctgtgtcc 180  
atctcccaga agctcctcat caatcaccat ctggccgaga c 221

<210> 235  
<211> 381  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 33  
<223> n = A,T,C or G

<400> 235  
ggtccaagaa agggacatct atgtgaaagt ganactgaga cagtgtctgtt cacaggtcat 60  
gctgcagaat aatacattcc caggcactgt cactgtgggg acccaagagg ccccaggagt 120  
gacctataac ctctccagaa agaccactct gtgtggcatc acagtccaca cagttaagg 180  
aaatattttag acttaacaat cagacaccag ctcttactca cacttacact cacagcccac 240  
acacaagtgt gcaaacatac acacacatat atatttcctg atacattcat ggaatatcag 300  
agccctgccc tgaagtcgtt agtgtctctg ctccccaac cgctgtctcc acattggcta 360  
agctccctca agagacctca g 381

<210> 236  
<211> 441  
<212> DNA  
<213> Homo sapiens

<400> 236  
aggtcctgtt gcccctttct tttgcccac ttgccattt ggggaattga atatttacc 60  
aacacctgta ctgcattgaa tattggaagc aaataacttg gctttgatct tataggctca 120  
cagatggagg aacgtacctt gaagttcaga tgagatttcg gacttttgag ttgatgctga 180  
aacagcttga gatttttggg gactactgag agatgataat tgtattgtgc aatatgagaa 240  
ggacatgaga tttggtgggc ataggtgtga aatgacattg tttggatgtg tttaccctcc 300  
aaatctcttg ttgaatgtga tcttaaactg tggtgggtgg cctagtggaa ggtgttgaat 360  
catgggggtg gactcttcat aatttgctta gctccatccc cttggtgatg agcaagtcct 420  
tgctctgttg tgtcacatga g 441

<210> 237  
<211> 281  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 81, 90, 194, 209, 210, 211, 219, 233  
<223> n = A,T,C or G

<400> 237  
tcctaaaaaa ttagctgacc ttgttaaaaa tgttggcgtg agcagtatat tattacctat 60

```

ctttttttat tgtgtgtgtg nggtgtgtgn ttaaactaat tggctgaaat atctgcctgt 120
ttccctcttt acatttttct tgtttctttc cttattttatc tttgtccatc ttgagatcta 180
ctgtaaagtg aatnttttaa tgaaaacann nccaagttnt actctcactg ggnttgggac 240
atcagatgta attgagaggc caacaggtaa gtcttcacgt c 281

```

&lt;210&gt; 238

&lt;211&gt; 141

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 30, 85

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 238

```

gtctgcctcc tcctactgtt tccctctatn aaaaagcctc cttggcgcag gttccctgag 60
ctgtgggatt ctgcactggg gcttnggatt ccttgatag ttccttcaaa tccactgaga 120
attaaataaa catcgctaaa g 141

```

&lt;210&gt; 239

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 29, 30, 65, 86, 471, 489

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 239

```

aacaatctaa acaaatccct cggttctann atacaatgga ttccccatat tggaaggact 60
ctgangcttt attccccac tatgcntatc ttatcatttt attattatac acacatccat 120
cctaaactat actaaagccc ttttcccatg catggatgga aatggaagat ttttttttaa 180
cttggtctag aagtcttaat atgggctgtt gccatgaagg cttgcagaat tgagtccatt 240
ttctagctgc ctttattcac atagtgatgg ggtactaaaa gtactgggtt gactcagaga 300
gtcgtgtgca ttctgtcatt gctgtactc taacactgag caacactctc ccagtggcag 360
atccccctgta tcattocaag aggagcattc atccctttgc tctaataatc aggaatgatg 420
cttattagaa aacaaactgc ttgacctcagg aacaagtggc ttagcttaag naaacttggc 480
tttgctcana tccctgatcc t 501

```

&lt;210&gt; 240

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 240

```

tgtcctgaaa ggccattact aatagaaaaca cagcctttcc aatcctctgg aacatattct 60
gtctgggttt ttaatgtctg tggaaaaaaa ctaaacaagt ctctgtotca gttaagagaa 120
atctattggt ctgaagggtt ctgaacctct ttctggttct cagcagaagt aactgaagta 180
gatcaggaa gggctgcctc aggaaaattc ctagatccta ggaattcagt gagaccctgg 240
gaaggaccag catgctaatac agtgtcagt aatccacagt ctttacttcc tgcctcataa 300
agggccaggt ctcccagta ccaagtcctt tcctcatgaa gttgtgttgc ctcaggctgt 360
ttaaggacca ttgctgtct tggtcacatg agtctgtctc cttacttttag tccctgggca 420
atccttgctt aatgcttttg ttgactcaac g 451

```

&lt;210&gt; 241

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 62, 82, 364, 370, 385

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 241

```
aatctccagt gtgatggtat cgggggttaga gcttcaatct ccagtgtgat ggtactgcag 60
cnagagcttc aatctccagt gngatggtat taggggttaga tcttcaatct ccagtgtgat 120
ggtatcaggg ttagagcttc agcctccagt gtgatggtat cagggttaga gcttcagcct 180
ccagtgtgat ggtatcgggg ttagatcttc aatccccagt ggtgggtggt agagcttcaa 240
tctccagtgt gatgtattg gggtagagc ttcaatctcc agtctgatgg tgttcggga 300
tggggctttt aagatgtaat tagggtttaa gatcataagg gacctggtct gatggggatt 360
agtncgcttn tatgaagaga cacangaggg cttgctctat ctctgactct c 411
```

&lt;210&gt; 242

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 242

```
ttcccccttca caacagtaga gacctacaca gtgaactttg gggacttctg agatcagcgt 60
cctaccaaga cccagccca actcaagcta cagcagcagc acttcccaag cctgctgacc 120
acagtcacat caccatcag cacatggaag gccctggtg tggaactga aaggaagggc 180
tggtcctgcc cctttgaggg ggtgcaaaca tgactgggac ctaagagcca gaggtgtgt 240
agaggctcct gctccacctg ccagtctcgt aagaaatggg gttgctgcag tgttgagta 300
ggggcagagg gagggagcca aggtcactcc aataaaacaa gctcatggca c 351
```

&lt;210&gt; 243

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 243

```
gtctgtgctt tatcaggaaa agcacaagaa tatgtttttc tacctaaaac cctcttctac 60
tttaaaaaatg gtttctgtaa tttttctatg tttttaaaat gtttttatgc ttttttttaa 120
acacgtaaaag gatggaacct aatcctctcc cgagacgcct cctttgtgtt aatgcctatt 180
cttacaacag agaaacaagt acattaatat aaaaacgagt tgattattgg ggtataaaat 240
a 241
```

&lt;210&gt; 244

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 244

```
ggtccagagc aatagcgtct gtggtgaagc gcctgcactc ctccggagac atgcctggct 60
tatatgctgc atccacataa ccatagataa aggtgctgcc ggagccacca atggcaaaag 120
gctgtcagat cagcattcct cccagggttc catatacctg acctccttca cgttggtccc 180
agccagctac catgagatgt gcagacaagt cctctcgata tttatagctg atatttttca 240
ccacatttgc agcagccaaa acaagtggag gttcctccag ttctatccca tggagctcca 300
g 301
```

&lt;210&gt; 245

&lt;211&gt; 391

&lt;212&gt; DNA

<213> Homo sapiens

<400> 245

```
ctgacactgc tgatgtgggc cggggggcgc cgaggcacia ctggtggcgc gaccattgag 60
gcacctggag ggtaggcagc ttgtgtgca gacaccacag agagagaaaa gttggatgga 120
gtggtgggaa taatcagggt ggcacactgt gcctagaagc ttccagggcc accaagagaa 180
tggaaggga aactacaaca ttcacaacag aaataggagt caattcactt agaccagaa 240
ctccagaaag ggggagtgtg ggaatctaca atttcaaagc cagctcgtgt ctacctagag 300
ccccaaactg cataagcacc aggattgtac accttagtcc ctcaagatag tttcaagtga 360
gcgtgcaatt cactcttaca gaggagggcc t 391
```

<210> 246

<211> 291

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 26, 80, 82, 185, 255, 259

<223> n = A,T,C or G

<400> 246

```
tcctccacag gggaagcagg aagttnagcc agcttcaggc tggaaactgc ccagggcaca 60
gagctggcaa ggtgcaaagn cntctgcaga atattcacca ggttgacaca gacctccaca 120
ttcagacata ttccaagctt ctggggctct cagggcccca gaatttcctg gtcttgggca 180
tggtncacaa gtcatttgtc ctctctcatt ttggaagggt ccatttggac ataaaatgca 240
agcgttctcg tgctncaatna taataggtcc cagcctgcac tgacacattt g 291
```

<210> 247

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 80, 110, 125, 245, 249, 279, 318, 336, 339, 455, 471

<223> n = A,T,C or G

<400> 247

```
cactgagtga atgagtatat aatttatgaa aacagaaaag tgctttggaa aaaaaaaaaag 60
acaacaggag tacatacagn gaacaaaaaa gagtgtacca ggaggagcan accctgaaca 120
gttanaacta tggaaatcgc tatgctttgt gttgtcacag gagttaaaat aggaataccc 180
tgcatacaat aaatatattat tggataaata actaagcctg ataccctttt caatgcgtta 240
tacanactnt atcatcacac cactaatcta agttctcana agttaaacat tacaagactt 300
cagaacaaca taggcgtntt tggtccatt taacanaana aggaccatag tgatcattta 360
atctctatga gtctgtctta tcttctggaa aaggggccta acaccatttc cttttgcaaa 420
aaggtagctg ccttgcttcc agttctacca tcctntagca acccatcttt n 471
```

<210> 248

<211> 551

<212> DNA

<213> Homo sapiens

<400> 248

```
ccatgggatc aggaatgggg tcaggtcagt tgacctgagc ataccatta aacatgttca 60
aatgtcccca tcccaccac tcacatgaca tggctcccga gccctgagat ctgtatccca 120
agaacctcag ttgagaaata ttatggcag cttcactgtt gctcaagagc ctgggtattg 180
tagcagcctg ggggcagggt gtccctaatt ttctccaagt tcttcacatc agccagaatc 240
```

```

ccatctatgc ttgtctccag caaatggagg tgcccctct gctgacgtgc cctctcttcc 300
agctctgaca tcatgggccg cagttggctg ttgatctggg tcttggtctg ggaaagcttc 360
tgctccagta agaccagccc ctcttcatct acactgagag gctgggtccat cagatgcagg 420
aggccgtcta atgtgttgag tgtgtcttgg attgtaaccc cagcgttctt ggcctctgta 480
tcaaccttct gggcttctgt aatcaccatc tgtactgcat ccatattcgt gtcgaactcc 540
agtccttcc t                                     551

```

&lt;210&gt; 249

&lt;211&gt; 181

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; 3, 96

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 249

```

atntccagag ggaccgtaag actggtacaa gtttacacca taagaggcga cgtgggtcagc 60
cacaatgtct tcacctccac aggggctcat cacgnggtc agggcaaggg ccccagcat 120
cagagctttg tttaggatca tcctcttccc aaggcagcct tagcagttgc tgacctgccc 180
g                                     181

```

&lt;210&gt; 250

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

```

tctgtagcta ggatgagctg gctctcaagc aaaagtttgt cttcctgggt ccatttgttg 60
ttatcacttg ttattgaatg tacatcacaa attaaagtct gcattgttg acgtaagaga 120
atgtgccgac tttggtaacc aggagatttc atgttactgg actgcctgta gtcacgtatt 180
tctgctatga cacatccgca atgaaaaata ttaacctgag atttttctag gagatcaacc 240
aaaataggag gtaattcttc tgcattccaa tattcaagca actctccttc ttcatagggc 300
agtcgaatgg tctcggaatc tgatccgttt tttcccctga gcattcagaga atatccctca 360
tttcctgggt atagattgac cactaaacat gacaaagtct cttgcataac aagcttctct 420
aacaagttca catttcttct taatttctta acttcagggt ctttttcaca ttcttcaata 480
tacaagtcac aaagtttttg aaatacagat tttcttccac ttgataggta ttctctttta 540
ggaggtctct g                                     551

```

&lt;210&gt; 251

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

```

tgtctgtctc cccatcctgg ttactatgag tcgtctttgg cagaaaggac cacagatgga 60
gagcttggca ctcgctccaa ctttgccgaa aagaggacaa ccaccaaagt agtaggtaaa 120
aacacaattt tagcagcagt gaaataaaaa gaggaagtga ggatggggcc aggccgcaac 180
tataattaaa ctgtctgttt aggagaagct gaatccagaa gaaacacaag ctgtaaagtg 240
agagaggaca gggagcaggg cctttggaga gcaggagagg acaggctgtc accaagcgct 300
gctcggactc tgccctgaaa gatttgaatt ggacactgtc cagtcacgtg tgtggcaaac 360
cgtactccaa gcacttttct caccgcagag gaaggagctg ccatggctgt acccctgaac 420
gtttgtgggg ccagcgatgt g                                     441

```

&lt;210&gt; 252

&lt;211&gt; 406

&lt;212&gt; DNA

<213> Homo sapiens

<400> 252

```

tttttttttg aacaagtaaa aatttcttta ttgctgaca ataagataac ctacagggaa 60
aacctgatga aatctattaa aaagttacta aaactaataa aagaatttag gaaggttata 120
gaatgtaaga ccaagacaca aaaatcaatt acatttctat ataatagcaa tgaacagata 180
ctgaaatttt aaaaactaaa tcattttaca aaagtatcac aatatgaaac actccgggat 240
aaattggata aaagatgtgc aagactgtac aaaagctaca aaacatttat gaaggaaatt 300
ggaagataga aacaagatag aaaatgaaaa tattgtcaag agtttcagat agaaaatgaa 360
aaacaagcta agacaagtat tggagaagta tagaagatag aaaaat 406

```

<210> 253

<211> 544

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 224

<223> n = A,T,C or G

<400> 253

```

gaaggagtgc agtagcaaag tcacacctgt ccaattccct gagctttgct cactcagcta 60
atgggatggc aaaggtggtg gtgctttcat cttcaggcag aagcctctgc ccacccccct 120
caagggtctg aggccagtt ctcattgctgc ccttgggtgg gcattctgta acagaggaga 180
acgtctgggt ggccgcagca gctttgctct gagtgcctac aaanctaatg cttggtgcta 240
gaaacatcat cattattaaa cttcagaaaa gcagcagcca tgttcagtca ggctcatgct 300
gcctcactgc ttaagtgcct gcaggagccg cctgccaaag tccccctcct acacctggca 360
cactggggtc tgcacaaggc tttgtcaacc aaagacagct tccccctttt gattgcctgt 420
agacttttga gccaaagaaac actctgtgtg actctacaca cacttcaggt ggtttgtgct 480
tcaaagtcac tgatgcaact tgaaaggaaa cagtttaatg gtggaaatga actaccattt 540
ataa 544

```

<210> 254

<211> 339

<212> DNA

<213> Homo sapiens

<400> 254

```

tggcattcag ggcagtgtct tctgcatctc ctaggaaacct cgggagcggc agctccggcg 60
cctggtagcg agaggcgggt tccggagatc ccggcctcac ttcgtccac tgtggttagg 120
ggtgagtcct gcaaatgtta agtgatttgc tcaagggtgc catttcgcag gaattggagc 180
ccaggccagt tctctgagcc tatcattagg gctaaaggag tgcgtgatca gaattggtgc 240
tggacgggtc tacttgtcct gcctgctgct ggggtccctg ggctctatgt gcacctctct 300
cactatctac tggatgcagt actggcgtgg tggctttgc 339

```

<210> 255

<211> 405

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 11, 39, 70, 87, 103, 120, 177, 181, 220, 229, 233, 341, 345, 366, 380, 402

<223> n = A,T,C or G

<400> 255

```

gagggtttttt nttttttttt tttttttttt caattaaana tttgatttat tcaagtatgt 60
gaaaacattn tacaatggaa acttttntta aatgctgcat gtncgtgtgt atggaccacn 120
cacatacagc catgctgttt caaaaaactt gaaatgccat tgatagtta aaaactntac 180
ncccgatgga aaatcgagga aaacaattta atgtttcatn tgaatccana ggngcatcaa 240
attaaatgac agctccactt ggcaaataat agctgttact tgatggtatc caaaaaaaaa 300
tggttgggga tggataaatt caaaaatgct tccccaagg ngggnggttt ttaaaaagtt 360
tcaggnccaca acccttgcan aaaacactga tgcccaacac antga 405

```

&lt;210&gt; 256

&lt;211&gt; 209

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 6

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 256

```

gggcangtct ggtcctctcc ccacatgtca cactctctcc agcctctccc ccaaccctgc 60
tctccctcct cccctgccct agcccaggga cagagtctag gaggagcctg gggcagagct 120
ggaggcagga agagagcact ggacagacag ctatggtttg gattggggaa gaggttagga 180
agtaggttct taaagaccct ttttttagta 209

```

&lt;210&gt; 257

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 306, 311, 343

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 257

```

tctggacacc ataatccctt ttaagtggct ggatgggtcac acctctccca ttgacaagct 60
gggttaagtc aataggttga ctaggatcaa cagcacccaa atcaataaga tactgcagtc 120
tattgagact caaaggctta tactggcgtc tgaaactatg tccttcgtta aaccctgatt 180
ttgggattcg gatgtaaaat ggagtctggc ctccctcaaa gcccaagcgg ggccgggttc 240
ctctttgcct ttctccttta tggcctctgc cacattttct acctcttctc cgacctcttg 300
gtcttntctc nggtttcttg gagccgggat tcggctttaa gtn 343

```

&lt;210&gt; 258

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 258

```

gcggttcttg acttctagaa gactaaggct ggtctgtgtt tgcttggttg cccacctttg 60
gttgataccc agagaacctg ggcacttgct gcctgatgcc caccctgcc agtcattcct 120
ccattcaccg agcgggagggt gggatgtgag acagcccaca ttggaaaatc cagaaaaccg 180
ggaacaggga tttgcccttc acaattctac tcccagatc ctctcccctg gacacaggag 240
acccacaggg caggacccta agatctgggg aaaggagggt ctgagaacct tgaggtagcc 300
ttagatcctt ttctacccac ttctctatgg aggattccaa gtcaccactt ctctcaccgg 360
cttctaccag ggtccaggac taaggcggtt tctccatagc ctcaacattt tgggaatctt 420
cccttaatca cccttgctcc tcctgggtgc ctggaagatg gactggcaga gacctctttg 480
ttgcggtttg tgctttgatg ccaggaatgc cgcctagtt 519

```

<210> 259  
<211> 371  
<212> DNA  
<213> Homo sapiens

<400> 259  
attgtcaact atatacacag tagtgaggaa taaaatgcac acaaaacaat ggatagaata 60  
tgaaaatgtc ttctaaatat gaccagtcta gcatagaacc ttcttctctt ccttctcagg 120  
tcttccagct ccatgtcatc taaccacatt acaaacgtg gacgtatcgc ttccagaggc 180  
cgtcttaaca actccatttc caaaagtcac ctccagaaga catgtatttt ctatgatttc 240  
ttttaaaca atgagaattt acaagatgtg taactttcta actctatttt atcatacgtc 300  
ggcaacctct ttccatctag aagggtctaga tgtgacaaat gttttctatt aaaaggttgg 360  
ggtggagtgtg a 371

<210> 260  
<211> 430  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 57, 189, 208, 256, 426  
<223> n = A,T,C or G

<400> 260  
ttggattttt tgacttgcca ttccagtttt ttactttttt tttttttttt ttttganaaa 60  
tactatatat attgtcaaag agtggtacat aggtgagtgt tcatcttccc tctcatgccg 120  
gtatactctg cttcgctgtt tcagtaaaag ttttccgtag ttctgaacgt cccttgacca 180  
caccataana caagcgcaag tcaactcanaa ttgccactgg aaaactggct caactatcat 240  
ttgaggaaag actganaaaag cctatcccaa agtaatggac atgcaccaac atcgcggtac 300  
ctacatgttc ccgtttttct gccaatctac ctgtgtttcc aagataaatt accaccagg 360  
gagtcacttc ctgctatgtg aacaaaaacc cggtttcttt ctggagggtgc ttgactactc 420  
tctcngagc 430

<210> 261  
<211> 365  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 178  
<223> n = A,T,C or G

<400> 261  
tcctgacgat agccatggct gtaccactta actatgattc tattccaact gttcagaatc 60  
atatcacaaa atgacttgta cacagtagtt tacaacgact cccaagagag gaaaaaaaaa 120  
aaaaaagacg cctcaaaaatt cactcaactt ttgagacagc aatggcaata ggcagcanag 180  
aagctatgct gcaactgagg gcacatatca ttgaagatgt cacaggagt taagagacag 240  
gctggaaaaa atctcatact aagcaaacag tagtatctca taccaagcaa aaccaagtag 300  
tatctgctca gcctgccgct aacagatctc acaatcacca actgtgcttt aggactgtca 360  
ccaaa 365

<210> 262  
<211> 500  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 262

```
cctagatgtc atttgggacc cttcacaacc attttgaagc cctgtttgag tccctgggat 60
atgtgagctg tttctatgca taatggatat tcgggggttaa caacagtccc ctgcttggt 120
tctattctga atccttttct ttcaccatgg ggtgcctgaa ggggtgctga tgcataatgt 180
acaatggcac ccagtgtaaa gcagctacaa ttaggagtggt atgtgttctg tagcatccta 240
tttaaataag cctattttat cctttggccc gtcaactctg ttatctgctg cttgtactgg 300
tgctgtact tttctgactc tcattgacca tattccacga ccattggtgt catccattac 360
ttgatcctac tttacatgtc tagtctgtgt ggttgggtgt gaataggctt ctttttacat 420
ggtgctgcca gccagctaa ttaatggtgc acgtggactt ttagcaagcg ggctcactgg 480
aagagactga acctggcatg 500
```

&lt;210&gt; 263

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 263

```
ctcagagagg ttgaaagatt tgcctacgaa agggacagtg atgaagctaa gctctagatc 60
caggatgtct gacttcaaat tgaaactccc aaagtaatga gtttggaagg gtggggtgtg 120
gcctttccag gatgggggtc ttttctgctc ccagcggata gtgaaacccc tgtctgcacc 180
tggttgggcg tgttgctttc ccaaaggttt ttttttagg tccgtcgtg tcttgtggat 240
taggcattat tatctttact ttgtctccaa ataacctgga gaatggagag agtagtgacc 300
agctcagggc cacagtgcga tgaggaccat cttctcacct ctctaaatgc aggaagaaac 360
gcagagtaac gtggaagtgg tccacaccta ccgccagcac attgtgaatg aca 413
```

&lt;210&gt; 264

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 264

```
tccaatgggg cctgagagc tgtgacagga actcacactc tggcactggc agcaaaacac 60
cattccaccc cactcatcgt ctgtgcacct atgttcaaac tttctccaca gttccccaat 120
gaagaagact catttcataa gtttgtggct cctgaagaag tcctgccatt cacagaaggg 180
gacattctgg agaaggtcag cgtgcattgc cctgtgtttg actacgttcc cccagagctc 240
attaccctct ttatctccaa cattggtggg aatgcacctt cctacatcta ccgcctgatg 300
agtgaactct accatcctga tgatcatgtt ttatgaccga ccacacgtgt cctaagcaga 360
ttgcttaggc agatacagaa tgaagaggag acttgagtgt tgctgctgaa gcacatcctt 420
gcaatgtggg agtgcacagg agtccaccta aaaaaaaaaa tccttgatac tgttgctgc 480
cttttttagtc accccgtaac aagggcacac atccaggact gtgt 524
```

&lt;210&gt; 265

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 265

```
tcctttcttc tacttcagga gatgattcaa agttacttgt ggacatttct ttaagttctg 60
aagacaaatg agacaggatt tggcctgcgg gttcttcaga cttctctacc acctccatta 120
actcttcacg ttggcttgac gtaggcaatg cactattttg ctcttttgtt tctggagatg 180
accagcacc acttctttct cttggcgggg ttctaagtgt gtctttgaat accagtgaag 240
actcaggcct atcctgtact ggaaaggac taaatttgtc tttctgtcta ggaggtgatg 300
cagtagcatc ctctgagggg ggtaaggcca ttttctcttt ttga 344
```

&lt;210&gt; 266

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
<221> misc\_feature  
<222> 78  
<223> n = A,T,C or G

<400> 266  
ccacaatgtc cataacttga gcaggctttg gcattcccacc acccccttca gaccaataca 60  
cactatgttg gaggaacnac tttaaaatgt aaaatgagaa atgggcactg aacactccat 120  
cctcactccc aacagcccac ccacacacct cttcaactgc tatccaaaca tggaggagct 180  
cttgtggaag agaggctcaa caccaaataa 210

<210> 267  
<211> 238  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 5, 19, 31  
<223> n = A,T,C or G

<400> 267  
tcggncctcc caccctctna ctgaaattct ntgaaattct cccctttggg atgaggatgg 60  
caaccccagg catgtaccct cccaacctgg gacccgacct aataccctaa catcctgctg 120  
acagtggctg ttctcgctgg gcaggcgctcc caaagcacat cgagccagat tcaggcagag 180  
tggaactggc cctcagcca tcagtggagg tggcctggga ggctctacc tgaacggg 238

<210> 268  
<211> 461  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 459  
<223> n = A,T,C or G

<400> 268  
tcctcaagga catgccctt gatagaaact cagttcctgt ctccagttcc ctctgggacc 60  
tgatccccca aatgcagggc ctgggactat atccagttcc ttattttcag aggcccatgc 120  
acaagatgca cagcaaataa gtgctgaata aagacccagc tactgctagc ttaccctgct 180  
ccaaacattc accaagtcct cagcaaagag ggccatccat tcacctcttc taaaaacaca 240  
ctgagctccc cagtctatac cccaagatat gcttggctcc caactatccc tcctctctca 300  
tctccaagcc agttccccct ttctaagtat actgatatta ccaaagacac tgacaatctt 360  
cttttcttac ctctccccag tgactagggt tgcagcagga gctctataag tcctagtata 420  
cagcagaagc tccataaatg tgtgctgacc taacattang c 461

<210> 269  
<211> 434  
<212> DNA  
<213> Homo sapiens

<400> 269  
ctgtgttggg gagcaccgat tccactcaa tatggcgtgg cttacagtct tcattaggtt 60  
cccgtccca accagaatga ggaatgatca cttcatctgt caaggcatgc agtgcagtgt 120  
ccacaatctc cattttgatt gagtcatggg atgaaagatt ccacagggtt ccggtaataa 180  
cttcagtaa gtcacatatc cgagccttcc gaagcaatcg cacaagggca ggcacacat 240

cacagttttt tatggcaatc ttgttatcct ggtcacgtcc aaaagagata ttcttgagag 300  
ctccacaggc tccaagggtgc acttcctttt tgggatgggc taacaatccc accagtactg 360  
ggatgccctt gagcttccgc acgtcagttc tcaccttggtc attgcggtag cataagtgtt 420  
gcagggtatgc aaga 434

<210> 270

<211> 156

<212> DNA

<213> Homo sapiens

<400> 270

ctgcaccagc gattaccagt ggcattcaaa tactgtgtga ctaaggattt tgtatgctcc 60  
ccagtagaac cagaatcaga caggtagtag ctagtcaaca gcaagtcttt gttggattcg 120  
agtaggtcca ggatctgctg aaggctcgag gaggta 156

<210> 271

<211> 533

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 100, 137, 383, 385, 411

<223> n = A,T,C or G

<400> 271

ccactgtcac ggtctgtctg acacttactg ccaaacgcat ggcaaggaaa aactgcttag 60  
tgaagaactt agaagctgtg gagaccttgg ggtccacgtn caccatctgc tctgataaaa 120  
ctggaactct gactcanaac cggatgacag tggccacat gtggtttgac aatcaaatcc 180  
atgaagctga tacgacagag aatcagagtgt gtgtctcttt tgacaagact tcagctacct 240  
ggcttgcctt gtccagaatt gcagggtcttt gtaacagggc agtgtttcag gctaaccagg 300  
aaaacctacc tattcttaag cgggcagttg caggagatgc ctctgagtca gcactcttaa 360  
agtgcataga gctgtgctgt ggntnctgtg aggagatgag agaaagatac nccaaaatcg 420  
tcgagatacc cttcaactcc accaacaagt accagttgtc tattcataag aaccccaaca 480  
catcggagcc ccaacacctg ttggtgatga agggcgcccc agaaaggatc cta 533

<210> 272

<211> 630

<212> DNA

<213> Homo sapiens

<400> 272

tggatatttt ctttttcttt tggatgtttt atactttttt ttottttttc ttctctattc 60  
ttttcttcgc cttcccgtag ttctgtcttc cagttttcca cttcaaaact ctatcttctc 120  
caaattgttt catcctacca ctcccaatta atctttccat ttctgtctgc gtttagtaaa 180  
tgcgttaact aggcttttaa tgacgcaatt ctccctgcgt catggatttc aagggtcttt 240  
aatcaccttc ggtttaatct ctttttaaaa gatcgcttc aaattatttt aatcacctac 300  
aacttttaaa ctaaacttta agctgtttta gtcaccttca ttttaattca aaagcattgc 360  
ccttctattg gtattaatto ggggtctctg agtcctttct ctcaattttc ttttaataac 420  
attttttact ccatgaagaa gcttcattct aacctccgtc atgttttaga aaccttttat 480  
cttttccttc ctcatgttac tcttctaagt cttcatattt tctcttaaaa tcttaagcta 540  
ttaaaattac gttaaaaact taacgctaag caatatotta gtaacctatt gactatattt 600  
tttaagtagt tgtattaatc tctatctttc 630

<210> 273

<211> 400

<212> DNA

<213> Homo sapiens

<400> 273  
tctgggtttgc cctccagttc attctgaatc tagacttgct cagcctaatc aagttcctgt 60  
acaaccagaa gcgacacagg ttcotttggg atcatocaca agtgaggggt acacagcatc 120  
tcaacccttg taccagcctt ctcatgctac agagcaacga ccacagaagg aaccaattga 180  
tcagattcag gcaacaatct ctttaaatac agaccagact acagcatcat catcccttcc 240  
tgctgcgtct cagcctcaag tatttcaggc tgggacaagc aaacctttac atagcagtgg 300  
aatcaatgta aatgcagctc cattccaatc catgcaaagc gtgttcaata tgaatgcccc 360  
agttcctcct gttaaatgaac cagaaacttt aaaacagcaa 400

<210> 274  
<211> 351  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 2  
<223> n = A,T,C or G

<400> 274  
tntgagtatg tcccagagaa ggtgaagaaa gcggaaaaga aattagaaga gaatccatat 60  
gaccttgatg cttggagcat tctcattcga gaggcacaga atcaacctat agacaaagca 120  
cggaagactt atgaacgcct tggtgccagc ttccccagtt ctggcagatt ctggaaactg 180  
tacattgaag cagaggttac tattttatct tttttttct tatatcagta ttgcagcatt 240  
cactgtagtg atagaaaaca agtttagaac atagccaatt aggacaagga ggatttaaat 300  
gtgtcttacc tttattttgt aaaataggta taaaggagta attaaaatga a 351

<210> 275  
<211> 381  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 4, 11, 12, 13  
<223> n = A,T,C or G

<400> 275  
gcgnggtcgc nnncgaggtc tgagaagccc ataccactat ttgttgagaa atgtgtggaa 60  
tttattgaag atacaggggt atgtaccgaa ggactctacc gtgtcagcgg gaataaaaact 120  
gaccaagaca atattcaaaa gcagtttgat caagatcata atatcaatct agtgtcaatg 180  
gaagtaacag taaatgctgt agctggagcc cttaaagctt tctttgcaga tctgccagat 240  
cctttaattc catattctct tcatccagaa ctattggaag cagcaaaaat cccggataaa 300  
acagaacgtc ttcatgcctt gaaagaaatt gttaagaaat ttcacctgt aaactatgat 360  
gtattcagat acgtgataac a 381

<210> 276  
<211> 390  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 5  
<223> n = A,T,C or G

<400> 276

gctcngactc cgccgggacc tgctcggagg aatggcgccg ccgggttcaa gcaactgtctt 60  
cctgttggcc ctgacaatca tagccagcac ctgggctctg acgcccactc actacctcac 120  
caagcatgac gtggagagac taaaagcctc gctggatcgc cctttcaciaa atttggaatc 180  
tgcccttctac tccatcgtgg gactcagcag ccttgggtgct caggtgccag atgcaaagaa 240  
agcatgtacc tacatcagat ctaaccttga tcccagcaat gtggattccc tcttctacgc 300  
tgcccaggcc agccaggccc tctcaggatg tgagatctct atttcaaag agaccaaaga 360  
tctgcttctg gcagacctcg gccgcgacca 390

<210> 277

<211> 378

<212> DNA

<213> Homo sapiens

<400> 277

tgaggaaactt tggggtagga cggtgtctgc tatctccagt tccacagacc caaccagtta 60  
cgatgggtttt ggaccattta tgccgggatt cgacatcatt ccctataatg atctgcccgc 120  
actggagcgt gctcttcagg atccaaatgt ggctgcgttc atggtagaac caattcaggg 180  
tgaagcaggc gttgttggtc cggatccagg ttacctaatg ggagtgcgag agctctgcac 240  
caggcaccag gttctcttta ttgctgatga aatacagaca ggattggcca gaactggtag 300  
atggctggct gttgattatg aaaatgtcag acctgatata gtcctccttg gaaaggccct 360  
ttctgggggc ttataccc 378

<210> 278

<211> 366

<212> DNA

<213> Homo sapiens

<400> 278

ggagggcaca ttcccttttca cctcagagtc ggtcggggaa ggccaccag ataagatttg 60  
tgaccaaaccc agtgatgctg tccttgatgc ccaccttcag caggatcctg atgccaaagt 120  
agcttgtaga actgttgcta aaactggaat gatccttctt gctggggaaa ttacatccag 180  
agctgctgtt gactaccaga aagtgggttc tgaagctgtt aaacacattg gatatgatga 240  
ttcttccaaa ggttttgact acaagacttg taacgtgctg gtagccttgg agcaacagtc 300  
accagatatt gctcaagggtg ttcatcttga cagaaatgaa gaagacattg gtgctggaga 360  
ccaggg 366

<210> 279

<211> 435

<212> DNA

<213> Homo sapiens

<400> 279

cctaagaact gagacttggt acacaaggcc aacgacctaa gattagccca gggttgtagc 60  
tggaagacct acaaccaag gatggaaggc ccctgtcaca aagcctacct agatggatag 120  
aggacccaag cgaaaaagat atctcaagac taacggccgg aatctggagg cccatgacct 180  
agaaccagg aaggatagaa gcttgaagac ctggggaaat cccaagatga gaaccctaaa 240  
ccctacctct tttctattgt ttacacttct tactcttaga tatttccagt tctcctgttt 300  
atctttaagc ctgattcttt tgagatgtac tttttgatgt tgccggttac ctttagattg 360  
acaagtatta tgccctggcca gtcttgagcc agctttaaat cacagctttt acctatttgt 420  
taggctatag tgttt 435

<210> 280

<211> 435

<212> DNA

<213> Homo sapiens

<400> 280

tctggatgag ctgctaactg agcacaggat gacctgggac ccagcccagc caccocgaga 60

```

cctgactgag gccttcctgg caaagaagga gaaggccaag gggagccctg agagcagctt 120
caatgatgag aacctgcgca tagtggtggg taacctgttc cttgccggga tggtgaccac 180
ctcgaccacg ctggcctggg gcctcctgct catgatccta cacctggatg tgcagcgtga 240
gccagacct gtccggggcg ccgctcgaaa ttccagcaca ctggcggccg ttactagtgg 300
atccgagctc ggtaccaagc ttggcgtaat catggtcata gctgtttcct gtgtgaaatt 360
gttatccgct cacaattcca cacaacatac gagccggaag cataaagtgt aaagcctggg 420
gtgcctaata agtga                                     435

```

&lt;210&gt; 281

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 281

```

catctgatct ataaatgcgg tggcatcgac aaaagaacca ttgaaaaatt tgagaaggag 60
gctgctgaga tgggaaaggg ctccctcaag tatgcctggg tcttgataa actgaaagct 120
gagcgtgaac gtggtatcac cattgatatc tccttgtgga aatttgagac cagcaagtac 180
tatgtgacta tcattgatgc cccaggacac agagacttta tcaaaaacat gattacaggg 240
acatctcagg ctgactgtgc tgtcctgatt gttgctgctg gtgttggtga atttgaagct 300
ggtatctcca agaattggga gaccgagag catgcccttc tggcttacac actgggtgtg 360
aaacaactaa ttgtcgggtg taacaaaatg gattccactg agccccctac agccagaaga 420
gatatgagga aattgttaag                                     440

```

&lt;210&gt; 282

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

```

tctgtggcgc aggagcccc tccccggga gctctgacgt ctccaccgca gggactggtg 60
cttctcggag ctcccactcc tcagactccg gtggaagtga cgtggacctg gatcccactg 120
atggcaagct cttccccagc gatggttttc gtgactgcaa gaagggggat cccaagcacg 180
ggaagcggaa acgaggcccg ccccgaaagc tgagcaaaga gtactgggac tgtctcgagg 240
gcaagaagag caagcacgcy cccagaggca cccacctgtg ggagtccatc cgggacatcc 300
tcatccaccc ggagctcaac gagggcctca tgaagtggga gaatcggcat gaaggcgtct 360
tcaagttcct cgcctccgag gctgtggccc aactatgggg ccaaaagaaa aagaacagca 420
acatgacctc cgagaagctg agccgggcca tgagggtacta ctacaaacgg gagatcctgg 480
aacgggtgga tggccggcga ct                                     502

```

&lt;210&gt; 283

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

```

<222> 130, 147, 221, 225, 242, 246, 261, 279, 292, 294, 298, 314,
323, 332, 339, 342, 343, 350, 351, 356, 361, 362, 368, 372,
375, 379, 380, 382, 387, 390, 392, 394, 401, 404, 406, 409,
413, 423, 431, 433

```

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 283

```

ccatattaga ttactggaac atctaagcat cagtgtgtga ccatgcgaac aaaagacttc 60
ggggagtgtc tattttttaa aaggtttatg tgtgtcgagg cagttgtaaa agatttactg 120
cagaatcaan cccactttta ggcttangac caggttctaa ctatctaaaa atattgactg 180
ataacaaaaa gtgttctaaa tgttgctatt ctgatccata nttgnttttt aaagaaaaaa 240
antgtntata cagaaagagt ntaaaagttc tgtgaattna atgcaaatta gncnccantc 300

```

ttgacttccc aaanacttga ttnatacctt tnactcctnt cnnttcctgn ncttcnttaa 360  
nntcaatnat tnggnagtnn anggcctctn gnanaacacc nttncncgnt ccncgcaatc 420  
cancgcctt nan 433

<210> 284

<211> 479

<212> DNA

<213> Homo sapiens

<400> 284

tctggaagga tcagggatct gagcaaagcc aagtttactt aagctaagcc acttggtcct 60  
gggtcaagca gtttggtttc taataagcat cattcctgat cattagagca aagggatgaa 120  
tgctcctctt ggaatgatac aggggatctg ccactgggag agtggtgctc agtggttagag 180  
tagcagcaat gacagaatga cagcgactct ctgagtcaac ccagtacttt tagtaccctg 240  
tactatgtg aataaaggca gctagaaaat ggactcaatt ctgcaagcct tcatggcaac 300  
agcccatatt aagacttcta gaacaagtta aaaaaaatc ttccatttcc atccatgcat 360  
gggaaaaggg ctttagtata gtttaggatg gatgtgtgta taataataaa atgataagat 420  
atgcatagtg ggggaataaa gcctcagagt ccttcagta tggggaatcc attgtatct 479

<210> 285

<211> 435

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 27, 83, 90, 93, 96, 184, 207, 227, 232, 293, 306, 307, 328,  
331, 339, 343, 347, 349, 350, 370, 371, 382, 383, 414, 418,  
434

<223> n = A,T,C or G

<400> 285

ttttttttt ttttttttt tcaatanaaa tgccataatt tattccattg tataaaaaag 60  
tcatccttat gtaacaaaat gtnttcttan aanaanaaat atattatttc aggtcataaa 120  
taatcagcaa acatacaact gttggcaact aaaaaaaaa ccaacactgg tattttccat 180  
cagngctgaa aacaaacctg cttaaanata tatttacagg gatagtnnag tntcaaaaa 240  
caaaaattga ggtatttttg ttcttctagg agtagacaat gacatttttg gangggcaga 300  
cccctnnccc aaaaaataaa ataagggnat nttcttcant atngaanann gggggcgccc 360  
cggggaaaaa naaaccttg gnnngggggt tggcccaagc ccttgaaaaa aaantttntt 420  
tcccaaaaaa aacng 435

<210> 286

<211> 301

<212> DNA

<213> Homo sapiens

<400> 286

cctgggttct ggtggcctct atgaatccca tgtaggggtg agaccgtact ccacccctcc 60  
ctgtgagcac caggtcaacg gctcccgcc cccatgcacg ggggaggag ataccccaaa 120  
gtgtagcaag atctgtgagc ctggctacag cccgacctac aaacaggaca agcactacgg 180  
atacaattcc tacagcgtct ccaatagcga gaaggacatc atggccgaga tctacaaaaa 240  
cgccccctg gagggagctt tctctgtgta ttcggacttc ctgctctaca agtcaggagt 300  
g 301

<210> 287

<211> 432

<212> DNA

<213> Homo sapiens

```

<400> 287
tccagcttgt tgccagcatg agaaccgcca ttgatgacat tgaacgccgg gactggcagg 60
atgacttcag agttgccagc caagtcagcg atgtggcggg acagggggac ccccttctca 120
acggcaccag ctttgccagc ggcaagggac accccagaa tggcgttcgc accaaactta 180
gatttatttt ctgttccatc catctcgatc atcagtttgt caatcttctc ttgttctgtg 240
acgttcagtt tcttgctaac cagggcaggc gcaatagttt tattgatgtg ctcaacagcc 300
tttgagacac ccttcccat atagcgagtc ttatcattgt cccggagctc tagggcctca 360
tagataccag ttgaagcacc actgggcaca gcagctctga agagacctt tgagggtgaag 420
agatcaacct ca 432

```

```

<210> 288
<211> 326
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 254
<223> n = A,T,C or G

```

```

<400> 288
tctggctcaa gtcaaagtcc tggctcctct ctccgcctcc ttcttcatca tagtaataaa 60
cgttgtcccc ggtgtcatcc tctgggggca gtaagggctc ttgaccacc gctctcctcc 120
gaagaaacag caagagcagc agaatcagaa ttagcaaagc aagaattcct ccaagaatcc 180
ccagaatggc aggaatttgc aatcctgctt cgacaggctg tgccttccta cagacgccgg 240
cggccccctc acantcacac acgtgacct ctaaggtggt cacttgggtt ttattctggt 300
tatccatgag cttgagattg attttg 326

```

```

<210> 289
<211> 451
<212> DNA
<213> Homo sapiens

```

```

<400> 289
gtcccgggtg ggctgtgccg ttggctcctgt gcggtcactt agccaagatg cctgaggaaa 60
cccagaccca agaccaaccg atggaggagg aggagggtga gacgttcgcc ttccaggcag 120
aaattgccca gttgatgtca ttgatcatca atactttcta ctogaacaaa gagatctttc 180
tgagagagct catttcaaat tcatcagatg cattggacaa aatccggtat gaaagcttga 240
cagatcccag taaattagac tctgggaaag agctgcata taaccttata ccgaacaaac 300
aagatcgaac tctcactatt gtggatactg gaattggaat gaccaaggct gacttgatca 360
ataaccttgg tactatcgcc aagtctggga ccaaagcgtt catggaagct ttgcaggctg 420
gtgcagatat ctctatgatt ggacctcggc c 451

```

```

<210> 290
<211> 494
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 421
<223> n = A,T,C or G

```

```

<400> 290
tttttttttt tcaaaacagt atatttttatt ttacaatagc aaccaactcc ccagtttgtt 60
tcaattgtga catctagatg gcttaagatt actttctggt ggtcacccat gctgaacaat 120
atttttcaat ctcccaaaca gcaaagactc aaaagagatt ctgcatttca catcagttca 180

```

```

caagttcaag agtcttccat ttatcttagc ttttgaata aattatcttt gaggtagaag 240
gacaatgacg aagccactta attccttggt tctgcataaa agcagattta ttcatacaaa 300
cttcatttat gtgaataaaag cagatgatga taaaatgttc tcttattctt gtttaaatcag 360
tagtggtagt gatgccagaa acttgtaaag gcaacttcaa ccaattgtgg ctcaagtgtg 420
ngtggttccc caaggctggt accaatgaga ctgggggttg ggaattagtt ggcatcatc 480
cctcctgctg ccca 494

```

<210> 291

<211> 535

<212> DNA

<213> Homo sapiens

<400> 291

```

tcgcgtgctt aacatgaaaa caaactttgt gctgtttggt tcattgtatg cattgatgga 60
gtcttgtctc tcacatggg gtgtctgacc atccaacctg cagtactcat aatttctcca 120
catgcaataa tcttccaaaa tgtccaatac ccttgctcatt tgactgaaga ttagtactcg 180
tgaaccttgt tcttttaact tagggagcag ctgttctaaa accaccattt tgccactgtt 240
ggttactaga tgcatactctg ttgtataagg tggaccaggt tctgctccat caaagagata 300
tggatgatta caacattttc tcaactgcat taggatgttc aataacctca ttttgtccat 360
ottgctgct gagttgagta tatctatatc cttcattaat atccgagtat accattccct 420
ttgcattttg ctgaggccca catagatttt tacttctctc tttggaggca aactcttttc 480
aacatcagcc ttaattcgac gaaggaggaa tggacgcaaa accatatgaa gcctc 535

```

<210> 292

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 4, 348

<223> n = A,T,C or G

<400> 292

```

tacnagcccc tgctgatcga gatcctggtg gaggtgatgg atccttcctt cgtgtgcttg 60
aaaattggag cctgcccctc ggcccataag cccttggttg gaactgagaa gtgtatatgg 120
ggcccaagct actggtgccg gaacacagag acagcagccc agtgcaatgc tgtcgagcat 180
tgcaaacgcc atgtgtggaa ctaggaggag gaatattcca tcttggcaga aaccacagca 240
ttgggttttt tctacttggt tgtctggggg aatgaacgca cagatctggt tgactttggt 300
ataaaaatag ggctccccca cctcccccat ttttgtgtcc tttattgnag cattgctgtc 360
tgcaaggagg ccccta 376

```

<210> 293

<211> 320

<212> DNA

<213> Homo sapiens

<400> 293

```

tcggctgctt cctggtctgg cggggatggg tttgctttgg aaatcctcta ggaggctcct 60
cctcgcatgg cctgcagtct ggcagcagcc ccgagttggt tcctcgctga tcgatttctt 120
tcctccaggt agagttttct ttgcttatgt tgaattccat tgccctcttt ctcatcacag 180
aagtgatggt ggaatcggtt cttttgtttg tctgatttat ggttttttta agtataaaca 240
aaagtgtttt attagcattc tgaaagaagg aaagtaaaat gtacaagttt aataaaaagg 300
ggccttcccc tttagaatat 320

```

<210> 294

<211> 359

<212> DNA

<213> Homo sapiens

<400> 294

```
ctgtcataaa ctggtctgga gtttctgacg actccttggt caccaaatgc accatttcct 60
gagacttgct ggcctctccg ttgagtcac ttggctttct gtcctccaca gctccattgc 120
cactgttgat cactagcttt ttcttctgcc cacaccttct tcgactgttg actgcaatgc 180
aaactgcaag aatcaaagcc aaggccaaga gggatgccaa gatgatcagc cattctggaa 240
tttggggtgt ccttatagga ccagagggtg tgtttgctcc accttcttga ctcccatgtg 300
agtgtccatc tgattcagat ccatgagtgg tatgggaccc cccactgggg tggaatgtg 359
```

<210> 295

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 558

<223> n = A,T,C or G

<400> 295

```
cctgagttgg gctgactgcc agagacagac ccctctgggt ctcggtgaac cagccaggca 60
tttacctcag tggttggcac ctggaacctg tccagggccc tcacctgact gaggagccgc 120
cgggcagtga agtaattgtc cagggtctatg ctcttggggg ggataccata gccatccaag 180
gtattcctca ggttggtgaa ctgggtctga gtataggcag aactgggccc caggatgatc 240
tcccggagtg ggggaagctg tgaggtcagg taagtatcca cgtccacccg taccccaatc 300
aaactcagca gaatggtgaa ctggagaagt ccttccgtta agtatttctt cagagaaagc 360
attgctgaag gaccagaatg tttatgcttt ttggttttta aaatcttcca aaagacaaat 420
caaggccact gctctgccgc tccagccagc aggttaccct cctcagtgtc aaaccccgta 480
cccaccctg gcagaacaca agggatgagc tccctgacgg cccagagga aagcacaccc 540
tgtggagcca aggccaanga cacactccag accacattca cttt 584
```

<210> 296

<211> 287

<212> DNA

<213> Homo sapiens

<400> 296

```
ccttatcatt cattcttagc tcttaattgt tcattttgag ctgaaatgct gcattttaat 60
tttaacaaa acatgtctcc tctctggtt ttgtagcct tcctccacat cttttctaaa 120
caagatttta aagacatgta ggtgtttggt catctgtaac tctaaaagat cttttttaa 180
ttcagtccta agaaagagga gtgctgtgcc cctaagagtg tttaatggca aggcagccct 240
gtctgaagga cacttcctgc ctaagggaga gtggtatttg cagacta 287
```

<210> 297

<211> 457

<212> DNA

<213> Homo sapiens

<400> 297

```
ccaattgaaa caaacagttc tgagaccgtt cttccaccac tgattaagag tgggggtggca 60
ggtattaggg ataataattca tttagccttc tgagctttct ggcagactt ggtgaccttg 120
ccagctccag cagccttctt gtccactgct ttgatgacac ccaccgcaac tgtctgtctc 180
atatcacgaa cagcaaagcg acccaaaggt ggatagtctg agaagctctc aacacacatg 240
ggcttgccag gaaccatata aacaatggca gcatcaccag acttcaagaa tttagggcca 300
tcttccagct ttttaccaga acggcgatca atcttttctt tcagctcagc aaacttgcat 360
gcaatgtgag ccgtgtggca atccaatata ggggcatagc cggcgcttat ttggcctgga 420
tggttcagga taatcacctg agcagtgaag ccagacc 457
```

<210> 298  
<211> 469  
<212> DNA  
<213> Homo sapiens

<400> 298  
tctttgactt tccttgtcta cctcctctgg agatctcaaa ttctccaggt tccatgctcc 60  
cagagatctc aatgattcct gattctcctc ttccaggagt ctgaatgtct cttgggtcac 120  
ttccacagac tccagtgggt cttgaatttc cttttctaga ggattcattg ccccttgatt 180  
tatttctctt ggagtcacac gtggtgcttg agtttctgga gatttcagtg ttccagggt 240  
ctcttgtccc gcagacttca gtgattctag gatctctgtt tctaaagatt ttactgcctc 300  
tatgtctctt tctttgagtg actttaagaa ctcttgattc tcattttcaa gaggtctagc 360  
tatctcctgg tcaagagact tcagtgggtc tagatccact ttttctgggg gtcttaaatgt 420  
catctgatcc tgttccccta gagacctccg tcgctgttga gtctctttt 469

<210> 299  
<211> 165  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 37, 82, 144  
<223> n = A,T,C or G

<400> 299  
tctgtggaga ggatgaggtt gagggaggtg gggatatntcg ctgctctgac cttaggtaga 60  
gtcctccaca gaagcatcaa antggactgg cacatatgga ctcccttcac aggccacaat 120  
gatgtgtctc tccttcgggc tggncggta tgcacagttg gggta 165

<210> 300  
<211> 506  
<212> DNA  
<213> Homo sapiens

<400> 300  
tctgaggaaa gtttgggctt attagtattt gctccagcga acctccaagt tttctccatt 60  
gcggaacaac taactaccag ctcccttggt cagtgggtcg cctccactca gaagtccca 120  
gtaggttctg tcattattgt tggcacatag gccctgaata caggtgatat agggcccca 180  
tgagcgctcc tccattgtga aaccaaatat agtatcattc attttctggg ctttctccat 240  
cacactgagg aagacagaac catttagcac agtgacattg gtgaaatatg tttcattgat 300  
tctcacagag taattgacgg agatatatga ttgtgagtca ggaggtgtca cagttatagg 360  
ctcatcagcg gagatgttga agttacctga agcagagacg caagaagagt ctttgtaaat 420  
atccaagaag gtctttccca tcagggcagg taagacctgg gctgcagcgt ttggattgct 480  
gaatgctcct tgagaaattt ccgtga 506

<210> 301  
<211> 304  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 221, 223, 252, 275, 280  
<223> n = A,T,C or G

<400> 301

```

tcctaaggca gagcccccat cacctoaggc ttctcagttc ccttagccgt cttactcaac 60
tgcccccttc ctctccctca gaatttgtgt ttgctgcctc tatcttggtt ttgtttttt 120
cttctggggg gggctctagaa cagtgcctgg cacatagtag gcgctcaata aatacttggt 180
tggtgaatgt ctctctctct tttccactct gggaaacctc ngnttctgcc attctgggtg 240
accctgtatt tntttctggt gccattcca ttgnccagn taatacttcc tcttaaaaat 300
ctcc 304

```

<210> 302  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

```

<400> 302
ttttcagtaa gcaacttttc catgctctta atgtattcct ttttagtagg aatccggaag 60
tattagattg aatggaaaag cacttgccat ctctgtctag gggtcacaaa ttgaaatggc 120
tcctgtatca catacggagg tcttggtgat ctgtggcaac agggagtttc cttattcact 180
ctttatttgc tgctgtttaa gttgccaacc tcccctccca ataaaaattc acttacacct 240
cctgcctttg tagttctggt attcacttta ctatgtgata gaagtagcat gttgctgcca 300
gaatacaagc attgcttttg gcaaattaaa gtgcatgtca tttcttaata cactagaaaag 360
gggaaataaa ttaaagtaca caagtccaag tctaaaactt tagtactttt ccatgcagat 420
ttgtgcacat gtgagagggg gtccagtttg tctagtgtat gttattttaga gagttggacc 480
actattgtgt gt 492

```

<210> 303  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

```

<400> 303
tctggggcag caggtactcc ctacggcact agtctacagg gggaaggacg ctctgtgctg 60
gcagcgggtg ctcacatggc ctgtctgcac tgtaaccaca ggctgggatg tagccaggac 120
ttggtctcct tggaagacag gtctgatgtt tggccaatcc agtccttcag accctgcctg 180
aaacttgtat cttacgtgaa cttaaagaat aaaatgcatt tctaccccca tctcgccccc 240
aggactggca cgacaggccc acggcagatt agatcttttc ccagtactga tcgggtgcgtg 300
gaattccagc caccacttct gattcgatc cacagtgatc ctgtcctctg agtattttaa 360
agaagccatt gtcaccccag tcagtgttcc aggagttggc aaccagccag taggggtgtg 420
cattctccac tcccagccc aggatgcgga tggcatggac ctcgcccgcg 470

```

<210> 304  
 <211> 79  
 <212> DNA  
 <213> Homo sapiens

```

<400> 304
tgtccattg ttaactcagc ctcaaactct aactgtcagg ccctacaaag aaaatggaga 60
gcctcttctg gtggatgag 79

```

<210> 305  
 <211> 476  
 <212> DNA  
 <213> Homo sapiens

```

<400> 305
tcaactgagcc accctacagc cagaagagat atgaggaaat tgtaaggaa gtcagcactt 60
acattaagaa aattggctac aaccccgaca cagtagcatt tgtgccatt tctggttga 120
atggtgacaa catgctggag ccaagtgtc acgtaagtgg ctttcaagac cattgttaa 180
aagctctggg aatggcgatt tcatgcttac acaaattggc atgcttgtgt ttcagatgcc 240
ttggttcaag ggatggaaag tcacccgtaa ggatggcaat gccagtggaa ccacgtgct 300

```

tgaggctctg gactgcatcc taccaccaac tcgtccaact gacaagccct tgcgcctgcc 360  
tctccaggat gtctacaaaa ttggtggtaa gttggctgta aacaaagtg aatttgagtt 420  
gatagagtac tgtctgcctt cataggtatt tagtatgctg taaatatttt taggta 476

<210> 306

<211> 404

<212> DNA

<213> Homo sapiens

<400> 306

tctgtctcgg agctcagggc gcagccagca cacacaggag cccacaggac agccacgtct 60  
tcacagaaac tacagaagtc aggacccagg cgaggacctc aggaacaagt gccccctgca 120  
gacagagaga cgcagtagca acagcttctg aacaactaca taataatgcg gggagaatcc 180  
tgaagaccac tgcattccac aagcactgac aaccacttca ggattttatt tcctccactc 240  
taacccccag atccatttat gagaagttag tgaggatggc aggggcatgg aggggtgaagg 300  
gacagcaagg atggctctgag ggcctggaaa caatagaaaa tcttcgtcct ttagcatatc 360  
ctggactaga aaacaagagt tggagaagag gggggttgat acta 404

<210> 307

<211> 260

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 10, 255, 257

<223> n = A,T,C or G

<400> 307

tcctgcctan acatctgtga gggcctcaag ggctgctgcc tcgactttct ccctagctaa 60  
gtccaccctg ccagggacac agccagggca ctgctctgtg ctgacttcca ctgcagccaa 120  
gggtcaaaat gaagcatctg cggaggccag gactccttgg catcgacac agtcagggga 180  
aaagccaccc tgactctgca ggacagaggg tctaggggtca tttggcagga gaacactggg 240  
gtgccaaggg aagcnanct 260

<210> 308

<211> 449

<212> DNA

<213> Homo sapiens

<400> 308

tctgtgctcc cgactcctcc atctcaggta ccaccgactg cactgggcgg ggccctctgg 60  
ggggaaaggc tccacggggc agggatacat ctgaggcca gtcactctct ggaggcagcc 120  
caatcaggtc aaagattttg cccaactggt cggcttcaga gtttccacag aagagaggct 180  
ttcgacgaaa catctctgca aagatacagc caaactoca catgtccaca ggtgttgcat 240  
atgtggactg cagaagaact tcgggagctc ggtaccagag tgtaacaacc ttgatcggtt 300  
cggctggcaa gcctggtggg ggtgccttgt ccagatatgt ccttaggtcc tggctacat 360  
gctcaaacac caggggttacc ttgatctccc ggtcagttcg ggatgtggca cagacgtcca 420  
tcagccggac aacattggga tgctcaaaa 449

<210> 309

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 384

<223> n = A,T,C or G

<400> 309

```
ctgtggaac ctggggtgcc gggtaaatgg agaactccag cttggatttc ttgccataat 60
caactgagag acgttccatg agcaggagg tgaaccaga accagttccc ccaccaaac 120
tgtggaaaac caagaagccc tgaagaccgg tgcactggtc agccagcttg cgaattcgg 180
ccaacacaag gtcaatgatc tccttgccaa tgggttagtg ccctcgggca tagttattgg 240
cagcatcttc cttgcctgtg atgagctgct cagggtggaa gagctggcgg taggtgccag 300
tgcgaacttc atcaatgact gtgggttcca agtctacaaa cacagcccgg ggcacgtgct 360
tgccagcgcc cgtctcactt gaanaagggt gtttgaagga agtcatctcc t 411
```

<210> 310

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 250

<223> n = A,T,C or G

<400> 310

```
tcctcgtcca gcttgactcg attagtcctc ataaggtaag caaggcagat ggtggctgac 60
cgggaaatgc ctgcctggca gtggacaaac acccttcctc cagcattctt gatggagtct 120
atgaagtcaa tggcctcggt gaaccaggag ctgatgtctg ccttggtggt gtcctccaca 180
gggatgctct tgtactggta gtgacctca aaatggttgg gacaattggc tgagacgttg 240
atcaaggcan ttatgcccac ggcacccagc atgtccttgc gggaagcgtg atacgcactg 300
cccaggtaca gaaagggcag
```

<210> 311

<211> 539

<212> DNA

<213> Homo sapiens

<400> 311

```
tctggcccat gaagctgaag ttgggagaga tgatgcttcg cctctgcttc acaaactcaa 60
aggcctcgtc cagcttgact cgattagtcc tcataaggta agcaaggcag atggtggctg 120
accgggaaat gcctgcctgg cagtggacaa acacccttcc tccagcattc ttgatggagt 180
ctatgaagtc aatggcctcg ttgaaccagg agctgatgtc tgccttggtg ttgtcctcca 240
cagggatgct cttgtactgg tagtgacct caaaatggtt gggacaattg gctgagacgt 300
tgatcaaggc agttatgccc aaggcatcca gcatgtcctt gcgggaagcg tgatacgcac 360
tgcccaggta cagaaagggc aggatttcca ccgggccacc ctgaaatcca gaaatatcca 420
acattcatca agcttgctca aagccaaggc cagtggccat acccacaata actttctgct 480
ggaaaagtca atttcagata ccgagtgaac tcagttctgt tgctggagga taaataaat 539
```

<210> 312

<211> 475

<212> DNA

<213> Homo sapiens

<400> 312

```
tcaaggatct tcctaaagcc accatgtgag aggattcgga cgagagtctg agctgtatgg 60
cagaccatgt cctgctgttc tagggatcat actgtgtgta ctctaaagtt gccactctca 120
caggggtcag tgataccac tgaacctggc aggaacagtc ctgcagccag aatctgcaag 180
cagcgctgt atgcaacgtt tagggccaaa ggctgtctgg tggggttggt catcacagca 240
taatggccta gtagtcaag gatccagggt gtgaggggct caaagccagg aaaacgaatc 300
ctcaagtcct tcagtagtct gatgagaact ttaactgtgg actgagaagc attttctctg 360
aaccagcggg catgtcggat ggctgctaag gcactctgca atactttgat atccaaatgg 420
```

agttctggat ccagttttcg aagattgggt ggcaactgtt taatgagaat cttea 475

<210> 313

<211> 456

<212> DNA

<213> Homo sapiens

<400> 313

tccacttaaa ggggtgcctct gccaaactggt ggaatcatcg ccacttccag caccacgcc 60  
 agcctaacat cttccacaag gatcccgatg tgaacatgct gcacgtgtt gttctggcg 120  
 aatggcagcc catcgagtac ggcaagaaga agctgaaata cctgccctac aatcaccagc 180  
 acgaatactt cttctgatt gggcgccgc tgctcatccc catgtatttc cagtaccaga 240  
 tcatcatgac catgatcgtc cataagaact ggggtggacct ggcctgggcc gtcagctact 300  
 acatccggtt cttcatcacc tacatccctt tctacggcat cctgggagcc ctccctttcc 360  
 tcaacttcat caggttcctg gagagccact ggtttgtgtg ggtcacacag atgaatcaca 420  
 tcgtcatgga gattgaccag gaggacctcg gcccg 456

<210> 314

<211> 477

<212> DNA

<213> Homo sapiens

<400> 314

tgcgtgggct tctggaagcc tggatctgga atcattcacc agattattct ggaaaactat 60  
 gcgtaccctg gtgttcttct gattggcact gactcccaca cccccaatgg tggcggcctt 120  
 gggggcatct gcattggagt tgggggtgcc gatgctgttg atgtcatggc tgggatcccc 180  
 tgggagctga agtgcccaa ggtgattggc gtgaagctga cgggctctct ctccggttg 240  
 tcctcaccca aagatgtgat cctgaagggt gcaggcatcc tcacggtgaa aggtggcaca 300  
 ggtgcaatcg tggaatacca cgggcctggt gtagactcca tctcctgcac tggcatggcg 360  
 acaatctgca acatgggtgc agaaattggg gccaccactt ccgtgttccc ttacaaccac 420  
 aggatgaaga agtatctgag caagaccggc cgggaagaca ttgccaatct agctgat 477

<210> 315

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 35

<223> n = A,T,C or G

<400> 315

caggtagctg atgtcaggtc tgcgaaactt cttanatttt gacctcagtc cataaaccac 60  
 actatcacct cggccatcat atgtgtctac tgtggggaca actggagtga aaacttcggt 120  
 tgctgcaggt ccgtgggaaa atcagtgacc agttcatcag attcatcaga atgggtgagac 180  
 tcatcagact ggtgagaatc atcagtgatc tctacatcat cagagtcggt cgagtcaatg 240  
 g 241

<210> 316

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 1, 4, 32, 39, 68, 77, 82, 94, 166, 172, 195, 196

<223> n = A,T,C or G

<400> 316  
nttntgtgat agtgtggttt atggactgag gncaaaatnt aagaagtttc gcagacctga 60  
catccaancc tgcccngcgc gncgctcgaa aggncgaatt ctgcagatat ccatacact 120  
ggcggccgct cgagcatgca tctagagggc ccaattcgcc ctatantgag tnatattaca 180  
attcactggc cgtcnnttta caacgtcgtg actgggaaaa ccctggcggt acccaactta 240  
a 241

<210> 317  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 15, 25, 135, 154, 193  
<223> n = A,T,C or G

<400> 317  
aggtaccctg ctcancagcc tggngcctg ggttgtctcc ttgtccatcc actgggccat 60  
tctgctctgc atttttttgt tcctcttttg gaggttccac tttgggttg ggctttgaaa 120  
ttatagggct acaantacct cggccgaaac cacnctaagg gcgaattctg cagatatcca 180  
tcacactggc ggncgctcga gcatgcatct agagggccca attcgcccta tagtgagtcg 240  
t 241

<210> 318  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 3, 5, 10, 11, 24, 28, 31, 34, 40, 42, 47, 53, 74, 80, 96,  
101, 127, 129, 136, 138, 205, 241  
<223> n = A,T,C or G

<400> 318  
cgngnacaan ntacattgat gganggtntg nggntctgan tntttantta cantggagca 60  
ttaatatattt cttnaacgtt cctcaccttc ctgaantaaa nactctgggt tgtagcgctc 120  
tgtgctnana accacntnaa ctttacatcc ctcttttga ttaatccact gcgcggccac 180  
ctctgccgcg accacgctaa gggcnaattc tgcagatata catcacactg gcggccgctc 240  
n 241

<210> 319  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 24, 36, 39  
<223> n = A,T,C or G

<400> 319  
caggtactga tcggtgcgtg gaantccagc caccantntt gattcgattc cacagtgatc 60  
ctgtcctctg agtatittta agaagccatt gtcaccccag tcagtgttcc aggagttggc 120  
aaccagccag tagggtgtgc cattctccac tccccagccc aggatgcgga tggcatggcc 180  
accatcatc tctccggtga cgtgttggtg cctcggccgc gaccacgcta agggcgaatt 240

c 241

<210> 320  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 27, 215, 216, 217, 220, 222, 235  
<223> n = A,T,C or G

<400> 320  
ggcaggtacc aacagagctt agtaatntct aaaaagaaaa aatgatcttt ttccgacttc 60  
taaacaagtg actatactag cataaatcat tctagtaaaa cagctaaggt atagacattc 120  
taataatttg ggaaaacctg tgattacaag tgaaaactca gaaatgcaaa gatgttggtt 180  
ttttgtttct cagtctgctt tagcttttaa ctctnnnaan cncatgcaca cttgnaactc 240  
t 241

<210> 321  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 2, 25, 26, 228  
<223> n = A,T,C or G

<400> 321  
angtaccaac agagcttagt aattnnntaaa aagaaaaaat gatctttttc cgacttctaa 60  
acaagtgact atactagcat aaatcattct agtaaaacag ctaagggtata gacattctaa 120  
taatttgagg aaacctatga ttacaagtga aaactcagaa atgcaaagat gttgggtttt 180  
tgttttctcag tctgcttttag cttttaactc tggaagcgca tgcacacntg aactctgctc 240  
a 241

<210> 322  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 322  
ggtaccaaca gagcttagta atttctaaaa agaaaaaatg atcttttttc gacttctaaa 60  
caagtgacta tactagcata aatcattctt ctagtaaaac agctaaggta tagacattct 120  
aataatttgg gaaaacctat gattacaagt aaaaactcag aaatgcaaag atgttggttt 180  
tttgtttctc agtctgcttt agcttttaac tctggaagcg catgcacact gaactctgct 240  
c 241

<210> 323  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 323  
cgagggtactg tcgtatcctc agccttggtc tatttcttta ttttagcttt acagagatta 60  
ggtctcaagt tatgagaatc tccatggctt tcaggggcta aacttttctg ccattctttt 120  
gctcttaccg ggctcagaag gacatgtcag gtgggatacg tgtttctctt tcagagctga 180  
agaaagggtc tgagctgcgg aatcagtaga gaaagccttg gtctcagtga ctccctggct 240

t 241

<210> 324  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 324  
agg tactgtc gtatcctcag ccttggttcta tttctttatt ttagctttac agagattagg 60  
tctcaagtta tgagaatctc catggctttc aggggctaaa cttttctgcc attcttttgc 120  
tcttaccggg ctcagaagga catgtcaggt gggatacgtg tttctctttc agagctgaag 180  
aaagggtctg agctgcggaa tcagtagaga aagccttggt ctcagtgact ccttggtttt 240  
c 241

<210> 325  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 325  
ggcagggtaca ttgtttttgc ccagccatca ctcttttttg tgaggagcct aaatacatto 60  
ttcctgggggt ccagagtccc cattcaaggc agtcaagtta agacactaac ttggcccttt 120  
cctgatggaa atatttcctc catagcagaa gttgtgttct gacaagactg agagagttac 180  
atgttgggaa aaaaaaagaa gcattaactt agtagaactg aaccaggagc attaagttct 240  
g 241

<210> 326  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 326  
gcagggtacat ttgtttttgcc cagccatcac tctttttttg gaggagccta aatacatto 60  
tcctgggggt ccagagtccc cattcaaggc gtcaagttaa gacactaac ttggcccttt 120  
ctgatggaaa tatttcctcc atagcagaag ttgtgttctg acaagactga gagagttaca 180  
tgttgggaaa aaaaaaagc attaacttag tagaactgat ccaggagcat taagtctga 240  
a 241

<210> 327  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 327  
ggtaccagac caagtgaatg cgacagggaa ttatttcctg tgttgataat tcatgaagta 60  
gaacagtata atcaaaatca attgtatcat cattagtttt ccaactgctc aactagtga 120  
gctgtgccaa gtagtagtgt gacacctgtg ttgtcatttc ccacatcag taagagcttc 180  
caaggaaagc caaatcccag atgagtctca gagagggatc aatatgtcca tgattatcag 240  
g 241

<210> 328  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 6, 19, 66, 232, 240

<223> n = A,T,C or G

<400> 328

```
ggtacnagac caaatgaang ccacagggaa ttatttcctg tgttgataat tcatgaagta 60
gaacantata atcaaaatca attgtatcat cattagtttt ccactgcctc acactagtga 120
gctgtgccaa gtagtagtgt gacacctgtg ttgtcatttc ccacatcacg taagagcttc 180
caaggaaagc caaatcccag atgagtctca gagagggatc aatatgtcca tnatcatcan 240
g 241
```

<210> 329

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 33, 61, 220, 228, 229, 240, 241

<223> n = A,T,C or G

<400> 329

```
ttcagggtcga gttggctgca gatttgtggt gcnttctgag cgtctgtcc tgcgccaaaa 60
ngcttcaaag tattattaaa aacatatgga tccccatgaa gccctactac accaaagtgt 120
accaggagat ttgatagga atggggctga tgggcttcac cgtttataaa atccgggctg 180
ctgataagaa gtaaggcttt gaaagcttca gcgcctgctn ctggtcanna ctaaccatan 240
n 241
```

<210> 330

<211> 241

<212> DNA

<213> Homo sapiens

<400> 330

```
ttttgtgcag atttgtggtg cgttctgagc cgtctgtcct gcgccaaagat gttcaaagt 60
attattaaaa acatatggat ccccatgaag ccctactaca ccaaagttta ccaggagatt 120
tggaataggaa tggggctgat gggcttcacg gtttataaaa tccgggctgc tgataaaaga 180
agtaaggctt tgaaagcttc agcgctgct cctggctcac actaaccaga tttacttga 240
g 241
```

<210> 331

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 1, 9, 41, 60, 61, 119, 124, 132, 139, 141, 153, 168

<223> n = A,T,C or G

<400> 331

```
nttttaggna ctttgggctc cagacttcac tggctctagg nattgaaacc atcacctggn 60
ntgcattcct catgactgag gttaacttaa aacaaaaatg gtaggaaagc tttcctatnc 120
ttcnggtaag anacaaatnt nctttaaaaa aangtggaag gcatgacnta cgtgagaact 180
gcacaaactg gccactgaca aaaatgacct ccatttgtgt gacttcattg agacacatta 240
c 241
```

<210> 332

<211> 241

<212> DNA

<213> Homo sapiens

<400> 332

```
tgtgaggaga gggaacatgc tgagaaactg atgaagctgc agaaccaacg aggtggccga 60
atcttccttc aggatatcaa gaaaccagac tgtgatgact gggagagcgg gctgaatgca 120
atggagtgtg cattacattt ggaaaaaat gtgaatcagt cactactgga actgcacaaa 180
ctggccactg acaaaaatga cccccatttg tgtgacttca ttgagacaca ttacctgaat 240
g 241
```

<210> 333

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 44, 52, 60, 98, 104, 108, 124, 126, 190, 198, 206, 214

<223> n = A,T,C or G

<400> 333

```
caggtacaag cttttttttt tttttttttt tttttttttt ttgnaaatat tntttattgn 60
aaatattcta tcctaaattc catatagcca attaatnttt acanaatntt ttgttaattt 120
ttgngngtat aaattttaca aaaataaagg gtatgtttgt tgcacacaac ttacaaataa 180
taataaaactn tttattgnaa atattnttta ttgnaaatat tctttatcct aaattccata 240
t 241
```

<210> 334

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 10, 16, 22, 24, 49, 158, 159, 237

<223> n = A,T,C or G

<400> 334

```
tacctgctgn aggggntgaa gncntctctg ctgccccagg catctgcanc ccctgctgct 60
ggttctgccc ctgctgcagc agaggagaag aaagatgaga agaaggagga gtctgaagag 120
tcagatgatg acatgggatt tggccttttt gattaaannc ctgctcccct gcaaataaag 180
cctttttaca caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagcttgtag ctgccnnggc 240
g 241
```

<210> 335

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 39

<223> n = A,T,C or G

<400> 335

```
ctatgtgctg ggatgactat ggagacccaa atgtctcana atgtatgtcc cagaaacctg 60
tggctgcttc aaccattgac agttttgctg ctgctggctt ctgcagacag tcaagctgca 120
gtcccccaa aggctgtgct gaaacttgag cccccgtgga tcaacgtgct ccaggaggac 180
tctgtgactc tgacatgccca gggggctcgc agccctgaga gcgactccat tcagtggctc 240
```

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c 241

<210> 336  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 336  
taccaaccta tgcagccaag caacctcagc agttcccac aaggccacct ccaccacaac 60  
cgaaagtatc atctcagggg aacttaattc ctgcccgtcc tgctcctgca cctcctttat 120  
atagttccct cacttgattt ttttaacctt ctttttgcaa atgtcttcag ggaactgagc 180  
taatactttt ttttttcttg atgttttctt gaaaagcctt tctgttgcaa ctatgaatga 240  
a 241

<210> 337  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 47, 56, 69, 228  
<223> n = A,T,C or G

<400> 337  
ggtactgtat gtagctgcac tacaacagat tcttaccgtc tccacanagg tcatanattg 60  
taaagtgttna ataactgactt tttttttatt cctttgactc aagacagcta acttcatttt 120  
cagaactggt ttaaaccctt gtgtgctggt ttataaaata atgtgtgtaa tccttggtgc 180  
tttcttgata ccagactgtt tcccgtggtt ggtagaata tattttgntt tgatgcttat 240  
a 241

<210> 338  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 338  
aggtacaggt gtgcgctgag ccgagtttac acggaaagga taaagcccat ttagtttctt 60  
ctcaaatgga gttttccact ttcctttgaa gtagacagca ttcaccagga tcctcctggt 120  
atccccatct acagaacctt caggtataaa gtttgaggatt ttgccttttg tttgagtcct 180  
gacccaggaa ttaatctttt ttctagcttc ttctgcacat tctaggaagt ctactgcctg 240  
g 241

<210> 339  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 339  
taccgacggc tcctggaggg agagagtga gggacacggg aagaatcaaa gtcgagcatg 60  
aaagtgtctg caactccaaa gatcaaggcc ataaccagg agaccatcaa cggaagatta 120  
gttctttgtc aagtgaatga aatccaaaag cagcgtgag accaatgaaa gtttccgcct 180  
gttgtaaaat ctattttccc ccaaggaaa tctttgcaca gacaccagtg agtgagttct 240  
a 241

<210> 340  
<211> 241  
<212> DNA

<213> Homo sapiens

<400> 340

```
gtagccctca cacacacatg cccgtaacag gatttatcac aagacacgcc tgcattgtaga 60
ccagacacag ggcgtatgga aagcacgtcc tcaagactgt agtattccag atgagctgca 120
gatgcttacc taccacggcc gtctccacca gaaaaccatc gccaaactct gcgatcagct 180
tgtgacttac aaacctgtgt taaaagctgc ttacatggac ttctgtcctt taaaagcttc 240
c 241
```

<210> 341

<211> 241

<212> DNA

<213> Homo sapiens

<400> 341

```
gtaccgccta ctttcgtctc atgtctccga acttcttget gatggccgtt ccaacgttgc 60
tgaaagctgc agttgccttt tgccctgcgt gactcaggtt ttcatgtgtt ttctttagg 120
cagtggtagt ctgcattgca tgccagcttt tgetgaagtt ctgttttaatt tcattcatca 180
ggttcatgcc gagttttgtt ttatctcaac tagatgcctt tctttcgtctg acaaaacttg 240
t 241
```

<210> 342

<211> 241

<212> DNA

<213> Homo sapiens

<400> 342

```
gtacattggt gctataaata taaatgctac ttatgaagca tgaaattaag cttctttttt 60
cttcaagttt tttctcttgt ctagcaatct gttaggcttc tgaaccaaga ccaaagttt 120
acgttcctct gctgcatacc aacgttactc caaacaataa aaatctatca tttctgctct 180
gtgctgagga atggaaaatg aaacccccac cccctgaccc ctaggactat acagtggaaa 240
c 241
```

<210> 343

<211> 241

<212> DNA

<213> Homo sapiens

<400> 343

```
gtacattggt tagcagtaat ttttttgaag caactgcact gacattcatt tgagttttct 60
ctcattatca gattctgttc caaacaagta ttctgtagat ccaaattggat taccagtgtg 120
ctacagactt cttattatag aacagcattc tattctacat caaaaatagt ttgtgtaagt 180
tagttttggt taccatctaa aatattttta aatgttcttt acataaaaat ttatgttggtg 240
t 241
```

<210> 344

<211> 241

<212> DNA

<213> Homo sapiens

<400> 344

```
ggtacaaaat tggttgaatt tagctaataa aaaaacatag taaatattta caaaaacgtt 60
gataacatta ctcaagtcac acacataata caatgtagac aggtcttaac aaagtttaca 120
aattgaaatt atggagattt cccaaaatga atctaatagc tcattgctga gcatgggtat 180
caatataaca tttaagatct tggatcaaat gttgtccccg agtcttctgc aatccagtcc 240
t 241
```

<210> 345

<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 345  
ggtagcgaagc tgagcgcacg ggggttgccc cagcgtggag cctggacctc aaacttcacg 60  
gaaaatgctc tctctctttg acaggcttcc agctgtctcc taatttcctg gatgaactct 120  
ccccggcgat ttaactgata ctgaaaagtg gtgagaggac tgaggaagac aaccagggtca 180  
gcgttagatc ggcctctgag ggtggtgccc ttgcctgagg agccaccctt taccaccttg 240  
g 241

<210> 346  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 346  
caggtaccac tgagcctgag atggggatga gggcagagag aggggagccc cctcttccac 60  
tcagttgttc ctactcagac tgttgcaactc taaacctagg gaggttgaag aatgagaccc 120  
ttaggtttta acacgaatcc tgacaccacc atctataggy tcccaacttg gttattgtag 180  
gcaaccttcc ctctctcctt ggtgaagaac atcccaagcc agaaagaagt taactacagt 240  
g 241

<210> 347  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 347  
aggtacatct aaaggcatga agcactcaat tgggcaatta acattagtgt ttgttctctg 60  
atggtatctc tgagaataact ggttgtagga ctggccagta gtgccttcgg gactgggttc 120  
acccccaggc ctgcggcagt tgtcacagcg ccagccccgc tggcctccaa agcatgtgca 180  
ggagcaaatg gcaccgagat attccttctg ccactgttct cctacgtggt atgtcttccc 240  
a 241

<210> 348  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 2, 18, 29, 35, 56, 57, 64, 76, 77, 85, 102, 103, 104, 189,  
232  
<223> n = A,T,C or G

<400> 348  
angtacttgg caagattnga tgctcttgng ctcantgaca tcattcataa cttgttnngtg 60  
tgancagagg aggagnncat catcntgtcc toattcgtca gnnncctctc ctctctgaat 120  
ctcaaacaag ttgataatgg agaaaaattt gaattctcag gattgaggct ggactgggttc 180  
cgctacang catacactag cgtggctaag gccctctctg accctgcatg anaaccctga 240  
c 241

<210> 349  
<211> 241  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 349

```
gcaggtagcca tttgtctgac ctctgtaaaa aatgtgatcc tacagaagtg gagctggata 60
atcagatagt tactgctacc cagagcaata tctgtgatga agacagtgt acagagacct 120
gctacactta tgacagaaac aagtgtctaca cagctgtggt cccactcgta tatgggtgtg 180
agacccaaat ggtggaaaca gccttaacct cagatgcctg ctatcctgac taatttaagt 240
c 241
```

&lt;210&gt; 350

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 350

```
aggtagctgt gatattttaa atatcacagt aacaagatca tgcttggtcc tacagtattg 60
cgggccagac acttaagtga aagcagaagt gtttgggtga ctttctact taaaattttg 120
gtcatatcat ttcaaaacat ttgcatcttg gttggctgca tatgctttcc tattgatccc 180
aaacccaaatc ttagaatcac ttcattttaa atactgagcg gtattgaata cttcgaagca 240
g 241
```

&lt;210&gt; 351

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 351

```
tacagaaatc atttggagcc gttttgagac agaagtagag gctctgtcaa gtcaatactg 60
cattgcagct tgggccactg aagaagccac gcctgagata caaaagatgc actacacttg 120
accgcgttta tgttgccttc ctctccctt ctctctcatc aactttatta gggttaaaaca 180
ccacatacag gctttctcca aatgactccc tatgtctggg gtttgggttag aattttatgc 240
c 241
```

&lt;210&gt; 352

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 10, 28, 29, 49, 54, 59, 72, 127, 148, 150, 160, 166, 182

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 352

```
gtaccctgtn gagctgcacc aagattannt ggggccatca tgactgcanc cacnacgang 60
acgcaggcgt gnagtgcctc gtctgacccg gaaacccttt cacttctctg ctcccagggt 120
gtcctcnggc tcataatgtg gaaggcanan gatctctgan gagttnccctg gggacaactg 180
ancagcctct ggagaggggc cattaataaa gctcaacatc attggcaaaa aaaaaaaaaa 240
a 241
```

&lt;210&gt; 353

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 353

```
aggtagcagt gcattaatctt gggcaaggaa agtgtcataa tttgatactg tatctgtttt 60
ccttcaaagt atagagcttt tggggaagga aagtattgaa ctgggggttg gtctggccta 120
ctgggctgac attaaactaca attatgggaa atgcaaaagt tggttggttg tggtagtgtg 180
tggttctctt ttggaatttt ttccaggtga ttaataata atttaaaact actataaaaa 240
```

c

241

&lt;210&gt; 354

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 1

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 354

```
ngcagggtccg ggcagggtacc aagattcatt ctcacaaaaa actagaaaca gaagggcaaa 60
ttccagtttc cttctgggat tgaatacttt caagtaagggt cttcgacaaa caatcagggg 120
gccaaattaat ccactgtaga ggtccttaac ttgatccaca gttgaataat aagcccatgg 180
aatacaagca gaatcctctg ttccagctcc agatctttct gggattttcc atacgtaagt 240
g                                     241
```

&lt;210&gt; 355

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

```
ggtacccacc ctaaatttga actcttatca agaggctgat gaatctgacc atcaaataag 60
ataggatgga cttttttttg agttcattgt ataaacaaat tttctgattt ggacttaatt 120
cccaaaggat taggtctact cctgctcatt cactctttca aagctctgtc cactctaact 180
tttctccagt gtcataagata ggggaattgct cactgcgtgc ctactctttc ttcacttacc 240
t                                     241
```

&lt;210&gt; 356

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 27

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 356

```
aggtagctgta attgagcatc cggaatntgg agaagtaatt tagctacagg gtgaccaacg 60
caagaacata tgccagttcc tcgtagagat tggactggct aaggacgatc agctgaagg 120
tcatgggttt taagtgtctg tggctcactg aagcttaagt gaggatttcc ttgcaatgag 180
tagaatttcc cttctctccc ttgtcacagg tttaaaaacc tcacagcttg tataatgtaa 240
c                                     241
```

&lt;210&gt; 357

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

```
ttttgtacca ccgatatgat caaggaaaat tctgccatt tttatggctg aagttctaaa 60
aacctaattc aaagttcttc catgatccta cactgcctcc aagatgggtcc aggctggcat 120
aaggcctgag cggcgggtgag atccgcggct gccagcagct tgcgctctt cagctggat 180
gaagcccttc ggccaccgga gtctccagga cctgcccggt cgccgctcga aagggcgaat 240
```

t 241

<210> 358  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 25, 57  
<223> n = A,T,C or G

<400> 358  
aggtacggg agtgggggtg aagcntgttc tctacatagg caacacagcc gcctaantca 60  
caaagtcagt ggtcggccgc ttcgaccaac atgtggtgag cattccacgg gcgcatgaag 120  
tctgggtgct gtgctcgagt ctctgaatat ttgatagga agcgacaaga aaattcaaac 180  
tgctctttgc tgactactgg aaagtgaaa gatgctcaag ttaccattc aaagaaacca 240  
t 241

<210> 359  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 359  
gaggtacaca aaaggaatac cttctgagag ccaggagtg aggaaaggg aaggagactt 60  
gacgtcaagg gtgcttttga ggaacatgac gggccagcca gcctgcccc actttgaggc 120  
cctgtggggc tctgtgact ataaatatac tgtctatttc taatgcaatc cgtctttcct 180  
gaaagatctt gttatctttt actattgaga catgctttca tttttgtggt cctgtttcca 240  
a 241

<210> 360  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 1  
<223> n = A,T,C or G

<400> 360  
ngtactctat actaattctg cttttttata cttaattcta aatttctccc ctctaattta 60  
caacaaattt tgtgattttt ataagaatct atgcctcccc aattctcaga ttcttctctt 120  
ttctccttta ttcttttgc taaattcagt ataagctttc ttggtatttt aggcttcagt 180  
cacattctta ttcctaaaca ccagcagttc ttcagagacc taaaatccag tataggaata 240  
a 241

<210> 361  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 361  
aggtactctc cgtgccccga cactgaacat tatccagcca gatctgcccc gtgccagctc 60  
ccactttgta cttttcttac tatcctgtct agaatcatgt ottatgattt taacagatat 120  
agaaccactc ctagaaaatg ttctttcact ttctcgtttc ctttttaatc tatcatcctg 180  
actactgaac ttaaaatctt tttcttcctt tttttgtttc tcttttcttt tatcctgttc 240

a

241

&lt;210&gt; 362

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 17, 23

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 362

```
aggtactttt atacctngct tangtcagtg acagatttac caatgacaac acaattttta 60
aattccaaca catatattac tttgtcctat gaagggcaaa aagtcaatat attttaaatt 120
ttaaaaacag aatggatata atgacctttt tacacatcag tgatatTTaa aagacttaaa 180
gagacaatac tatggttgag aactggctt cctattccag ccctaattaa agaaaaaata 240
g                                     241
```

&lt;210&gt; 363

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 4

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 363

```
ttangtacta aaaacaaaat cctaattctg ttttaaagag ctgggagatg ttaatcatat 60
gttcagtttt tccacgttat aatttcctaa atgcaaactt ttcaatcagg gcagttcaaa 120
ttcattacat cacagtaaat aacagtagcc aactttgatt ttatgcttat aggaaaaaaa 180
atcctgtaga tataaaaaca gcaaattttg acaataaaaa ctcaaaccat tcatccctaa 240
a                                     241
```

&lt;210&gt; 364

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 364

```
ggtacaagca gttagtcttg aaggcccttg ataagaatgt catcttctcc ccactgagca 60
tctccaccgc cttggccttc ctgtctctgg gggcccataa taccaccctg acagagattc 120
tcaaaggcct caagtccaac ctcacggaga cttctgaggc agaaattcac cagagcttcc 180
agcacctcct gcgcaccctc aatcagttca gcgatgagct gcagctgagt atgggaaatg 240
c                                     241
```

&lt;210&gt; 365

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 365

```
cgagggtactg agattacagg catgagccac cagcccggc caaaaacatt taaaaaatga 60
ctgtccctgc tcaaatactg cagtaggaaa tgtaatttga catatatcac ttccagaaaa 120
aaactttaaa tctttctata aaatgaattt gatacatcat cagcatgaag tgaagttaaa 180
atctcttaca aagtaaattc aggtatatca acaatgagat ccaaagtat cggttcaaga 240
```

t 241

<210> 366  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 366  
ggcagggtaca catcaaacac ttcatcgcct aaatgcaggg acatgcttcc atctgaccac 60  
ttgactatcc gagcattgct ttctttaatt tcatttcctt cttcatctcg gcgtatcctc 120  
catcttatag tattttctac ctttaatttt aacctgggtc taccttcttc atccagcatt 180  
tcttcacatt caaattcatc ttcataatac tgggctctac acttgagaaa gttgggcagt 240  
t 241

<210> 367  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 25  
<223> n = A,T,C or G

<400> 367  
gcagggtacaa ataattcctg ttgtnacatt tagtggagcg gattatctgt atacctcaaa 60  
ttttaattta agaaagtatc acttaaagag catctcattt tctatagatt gaggcttaat 120  
tactgaaaag tgactcaacc aaaaagcaca taacctttta aaggagctac acctaccgca 180  
gaaagtcaga tgccctgtaa ataactttgg tctttcaaaa tagtggcaat gcttaagata 240  
c 241

<210> 368  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 368  
tttgtacttt gttaatagtg accctcggag gaaatggatt tctcttctat taaaaactct 60  
atgggtatata agcattacat aataatgcta cttaaccacc ttttgtctca agaattatca 120  
ccaaagtttt ctggaaataa gtccacataa gaattaaata tttaaaaggt gaaatgttcc 180  
ttattttaac tttagcaaga tcttttcttt ttcattaaga aacactttaa taattttaaa 240  
g 241

<210> 369  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 369  
gcagggtactt tattcttatt tcttatccta tattctgtgt tacagaaaaa ctactaccat 60  
aaacaaaaca ccaaccagcc acagcagttg tgtcaagcat gacaattggc ctagtcttca 120  
cattttatta gtaagtctat caagtaagag atgaagggtc tagaaaaacta gacacaaagc 180  
aaccagggtc caaatcacca aggtagatct gtgcttagct aaaggggaaac acccgaagat 240  
t 241

<210> 370  
<211> 241  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 1

<223> n = A,T,C or G

<400> 370

```
ngttcacagt gccctccgg cctcgccatg aggtcttcc tgcgctccc ggtcctggtg 60
gtggttctgt cgatcgtctt ggaaggccca gcccagccc aggggacccc agacgtctcc 120
agtgccttgg ataagctgaa ggagtttgga aacacactgg aggacaaggc tcgggaactc 180
atcagccgca tcaaacagag tgaactttct gccaaagtgc gggagtgggt ttcagaagac 240
a 241
```

<210> 371

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 227

<223> n = A,T,C or G

<400> 371

```
ggcaggtcat cttgagcctt gcacatgata ctcagattcc tcacccttgc ttaggagtaa 60
aacaatatac ttacaggggt gataataatc tccatagtta ttgaaagtgg cttgaaaaag 120
gcaagattga cttttatgac attggataaa atctacaaat cagccctcga gttattcaat 180
gataactgac aaactaaatt atttccttag aaaggaagat gaaaggnagt ggagtgtggt 240
t 241
```

<210> 372

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 26, 27, 59

<223> n = A,T,C or G

<400> 372

```
aggtagagca aagcgaccct tggatgnata gatcagacgg aaattctctc ccgtcttgnc 60
aatgctgatg acatccatga atccagcagg gtagggtata tcagttcgga ccttgccatc 120
gattttaatg aaccgctgca tgcaaatctt ctttacttca tctcctgtca gggcatactt 180
aagtctgttc ctcaggaaaa tgatgagggg gagacactct ctcaacttgt ggggaccggg 240
g 241
```

<210> 373

<211> 241

<212> DNA

<213> Homo sapiens

<400> 373

```
tactgaaaca gaaaaaatgt attcccacaa aagctgttac acagcggttt ccggtcccca 60
gaagcagtag aaaaatcttag cattccaatg gaaggcatgt atttgtaaaa tattctaaaa 120
tcagctctat agtttccttg tctcttttga taagggatca gacagagggt gtgtccccc 180
tcagcagcta cccttcttga caaactggtc tccaataata cctttcagaa acttacaaga 240
```

c 241

<210> 374  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 374  
caggtactaa aacttacaat aaatatcaga gaagccgtta gtttttacag catcgtctgc 60  
ttaaagcta agttgaccag gtgcataatt tcccatcagt ctgtccttgt agtaggcagg 120  
gcaatttctg ttttcatgat cggaatactc aaatatatcc aaacatcttt ttaaaacttt 180  
gatttatagc tcctagaaaag ttatgttttt taatagtcac tctactctaa tcaggcctag 240  
c 241

<210> 375  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 375  
aggtacaaaag gaccagtatc cctacctgaa gtctgtgtgt gagatggcag agaacggtgt 60  
gaagaccatc acctccgtgg ccatgaccag tgctctgccc atcatccaga agctagagcc 120  
gcaaattgca gttgccaata cctatgcctg taaggggcta gacaggattg aggagagact 180  
gcctattctg aatcagccat caactcagat tgttgccaat gccaaaggcg ctgtgactgg 240  
g 241

<210> 376  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 376  
ggtacatttt actttccttc tttcagaatg ctaataaaaa acttttgttt atacttaaaa 60  
aaaccataaa tcagacaaac aaaagaaacg attccaacat cacttctgtg atgagaaaag 120  
aggcaatgga attcaacata agcaaagaaa actctacctg gaggaagaa atcgatcagc 180  
gaagaaacaa ctcggggctg ctgccagact gcaggccatg cgaggaggag cctcctagag 240  
g 241

<210> 377  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 234  
<223> n = A,T,C or G

<400> 377  
tccttttctgt ccaggtgatt cacagactag acctttctta tcctcctcct agagttttga 60  
cttgggactc tagtgtaag atgatgagcc cgtgcatcag gtccttctgc actttggtgg 120  
aagtctccca gggtaggttt cctatttgaa acagtggaat catgtttcca gtgataaagt 180  
ttaatgacct catccttttt ttttttttcc tcatctgcca tttgtgtgtc ttanatgggt 240  
t 241

<210> 378  
<211> 241  
<212> DNA

<213> Homo sapiens

<400> 378

```
aggtcagcga tcaggtcctt tatgggcagc tgctgggcag cccacaagc ccagggccag 60
ggcactatct ccgctgcgac tccactcagc ccctcttggc gggcctcacc ccagcccca 120
agtcctatga gaacctctgg ttccaggcca gccccttggg gaccctggta accccagccc 180
caagccagga ggacgactgt gtctttgggc cactgctcaa cttccccctc ctgcagggga 240
t                                                                 241
```

<210> 379

<211> 241

<212> DNA

<213> Homo sapiens

<400> 379

```
tacggagcaa tcgaagaggc atatccacac ttgggggtggc tatagggtctg gaaaatgctg 60
aagatgactg ctttactga ggtcaaggat tgtaatatgt ccagctttgt aaagccatta 120
aagcagaagt ttcttcagt atcttctctc taagaaacac catcacctcc atgtgcctta 180
cagaggcccc ctgcgttctg ctgcattgct tttgcgcaat cccttgatga tgaagatggt 240
c                                                                 241
```

<210> 380

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 24, 25, 26, 34, 36, 56, 113, 129, 137, 184, 185, 208, 210, 237, 240

<223> n = A,T,C or G

<400> 380

```
acgtacacgc agaccgacat gggnnnttca ggcntnagat caaactcaaa acctgnaatg 60
atatccactc tctttttctt aagctcaggg aaatatcca agtagaagtc canaaagtca 120
tcggctaana tgcttongaa tttgaattca tgcacatagg ccttgaaaaa actgtcaaac 180
tgannctgat caccaccaa gtgggcentn tatgacaaa agcagaaacc tttctcntan 240
g                                                                 241
```

<210> 381

<211> 241

<212> DNA

<213> Homo sapiens

<400> 381

```
aggtacaact taatggatta gcttttgggt ttaactgaat atatgaagaa attgggtctg 60
tctaaagaga gggatattca tatggctttt agttcacttg tttgtatttc atcttgattt 120
ttttcttttg aaaataaagc attctatttg gttcagattt ctcagatttg aaaaaggctc 180
tatctcagat gtagtaaatt atttcctttc agtttgtgaa agcaggattt gactctgaaa 240
g                                                                 241
```

<210> 382

<211> 241

<212> DNA

<213> Homo sapiens

<400> 382

```
gtactgctat aatcaatacg tctgatagac aggtttatcc actatatattga ccctacctct 60
```

aaaaggattg tcataattta tatgctttat gtttacacct atgatacagt tgccttgga 120  
cacaaaattt ttcattgtaa ttaaaaaaag aagagttgtg cagacagaag aaatcaaac 180  
taagaaaatc acaggagtag ataaatactc tagaattcat atacccttg aagatgggtt 240  
t 241

<210> 383

<211> 241

<212> DNA

<213> Homo sapiens

<400> 383

ggcaggtaca aagcttcttc tttgcttttt ataattttta agcaaataac acatttaact 60  
gtatttaagt ctgtgcaaat aatccttcag aagaaatata caagattctg tttgcagagg 120  
tcattttgtc tctcaaagat gattaaatga gtttgccttc agataaagtg ctcctgtcca 180  
gcagaactca aaaggccttc aagctgttca gtaagtgtag ttcagataag actccgtcat 240  
a 241

<210> 384

<211> 241

<212> DNA

<213> Homo sapiens

<400> 384

ggtacacaaa atacacttgc aagcttgctt acagagacct gttaaacaaa gaacagacag 60  
attctataaa atcagttata tcaacatata aaggagtgtg attttcagtt tgttttttta 120  
agtaaatatg accaaactga ctaaataaga aggcaaaaca aaaaattatg cttccttgac 180  
aaggcctttg gagtaacaaa aatgctttta ggctcctggt gaatgggggt gcaaggatga 240  
a 241

<210> 385

<211> 241

<212> DNA

<213> Homo sapiens

<400> 385

ggcaggtcta caatggtctt gtcccttctg tggaaatcgtt acaccaagag gtctcagtc 60  
tggtccctga cccacagtg agctgttttag atgaccttc acatcttcct gatcaactgg 120  
aagacactcc aatcctcagt gaagactctc tggagccctt caactctctg gcaccaggta 180  
ggtttgagg cttatgtccct ttaacttata catgcagagt agccaaactt tacctgaaa 240  
a 241

<210> 386

<211> 241

<212> DNA

<213> Homo sapiens

<400> 386

aggtaccttt ttcctctcca aaggaacagt ttctaaagt ttctgggggg aaaaaaact 60  
tacatcaaat ttaaaccata tgttaaactg catattagtt gtgttacacc aaaaaattgc 120  
ctcagctgat ctacacaagt ttcaaagtca ttaatgcttg atataaattt actcaacatt 180  
aaattatctt aaattattaa ttaaaaaaaa aactttctaa gggaaaaata aacaaatgta 240  
g 241

<210> 387

<211> 241

<212> DNA

<213> Homo sapiens

<400> 387  
accccactgg ccgctgtgga gtatctccac tctcccctcg tgagggccgc tcccaccgac 60  
cagtcgaact ttcgtaaagt gagttaatgt gttccactc cctttttccc ctttctggcc 120  
ttttgggtcca gaatttcctg gccttccggc atatcctggg agtcctcgac ttccaggaaa 180  
gccaatgtct ccccgatcac cttaagacc cggaggacct attggacctg gaaatcctcg 240  
t 241

<210> 388  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 388  
tttgtactct tgtccacagc agagacattg agtataccat tggcatcaat gtcaaaagtg 60  
acttcaatct gaggaacacc tcggggtgca ggaggtatgc ctgtgagttc aaacttgcca 120  
agcaggttct tatcctttgt catggcacgc tcgccttcat aaacctgaat aagtacacca 180  
ggctggttct cagaataggt agtgaaggtc tgtgtctgct tggtaggaat ggtggtatta 240  
c 241

<210> 389  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 6, 28, 38, 43  
<223> n = A,T,C or G

<400> 389  
tacctntgtt agtgagcacc ttgtcttntg tgcttatntc ttnaagataa atacatggaa 60  
ggatgtgaaa atcggaacac caactatgtg tctcactgca tctaagttaa gcagccacag 120  
ctgtgagagt ttcaaagca gaaagatgct gatgtgacct ctggaattca gacatactga 180  
gctatgggtc agaagtgttt tacttaaaaa gcaaacaatc cccaggaaat actgaatagg 240  
a 241

<210> 390  
<211> 241  
<212> DNA  
<213> Homo sapiens

<400> 390  
gcaggtacat ccacatgttc ctccaaatga cgtttggggc cctgcttgcc aacattcttt 60  
attgccagct gtcagggtgt catcttatct tcttcttcta cagccttatt gtaattcttg 120  
gctaattcca acatctcttt taccactgat tcattgcgtt tacaatgttc actgtagtcc 180  
tgaagtgtca aaccttccat ccaactcttc ttatgcaaatt tagcaacat cttctgttcc 240  
a 241

<210> 391  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 2, 10, 14, 22, 23, 25, 40, 50, 57, 59, 65, 71, 72, 73, 76,  
77, 78, 82, 83, 84, 95, 98, 100, 101, 102, 107, 148, 152,  
155, 158, 163, 169, 170, 172, 180, 182, 192, 193, 198, 200,

202, 203, 206, 207, 208, 213, 214, 218, 220, 224, 225

<223> n = A,T,C or G

<221> misc\_feature

<222> 235, 236

<223> n = A,T,C or G

<400> 391

```
cnnggcacaan cttntgtttt tnnntntttt tttttttttn tctttatttn tttttantnt 60
taaanaaaaa nnntannnaa annnggggtt aaatnctntn nncagancat taaaactgaa 120
ggggaaaaaa aaaccaaaaa cgagcttntt anttnacntg ggnttgggnn gntgctgatn 180
tnaagaagca anntttanan cnngcnnnat ganngagnn tcannttgaa atttinnacc 240
t                                                                 241
```

<210> 392

<211> 241

<212> DNA

<213> Homo sapiens

<400> 392

```
gaggtactaa atgggtatcct tagattaaaa ttttgtgctt gataacagct gttttttcta 60
cattagaaat aagatgccac acaaggaact acattccaga tttaaagaaa tgaaaggata 120
ccattagtgt gtataacaga ttattgttca tacttgtaaa gcattcttatg tcattgagaa 180
tataaagaac agtgccttag aagacagtga aaggtaagct ctagcttaat gtctatgatt 240
t                                                                 241
```

<210> 393

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 57, 75, 224

<223> n = A,T,C or G

<400> 393

```
ggcaggtaca taagcataat cagttatgga cagcttcttg tataaattgc tattcancaa 60
tacataaact gcctnaaaga tttatgctta caggtagaca ttcaatttac caataaaaca 120
gcatgttctg aaaatatggg cacattttaa aacatattaa gacagttctg ttaaccataa 180
tagtcccaca gtatgactga gtaataagaa tctacttcaa aagnaaaaaa aaaattaatc 240
a                                                                 241
```

<210> 394

<211> 241

<212> DNA

<213> Homo sapiens

<400> 394

```
aggtagagca gcagtagatg gctgcaacaa ccttcctcct accccagccc agaaaatatt 60
tctgccccac cccaggatcc gggacaaaa taaagagcaa gcaggcccc ttcactgagg 120
tgctgggtag ggctcagtgc cacattactg tgctttgaga aagaggaagg ggatttggtt 180
ggcactttta aaatagagga gtaagcagga ctggagaggc cagagaagat accaaaattg 240
g                                                                 241
```

<210> 395

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 1, 5, 8, 9, 14, 24, 26, 28, 32, 42, 54

<223> n = A,T,C or G

<400> 395

```
nggcnggnnc caanatatga aatntnanta tnatacatga tnaaaagctt tatntatntt 60
agtgaagtaat taagttttaca ctgtgaataa ggattaattc ccagatgacc atctacagtt 120
actaccacat agagggtata cacggatgga tcgattacaa gaataataaaa cttattttcc 180
ttcctgtatc cacatttctt tgcaatgtga atttgcaggc cctctcaaga agtggagtct 240
a                                                                 241
```

<210> 396

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 26

<223> n = A,T,C or G

<400> 396

```
gaggtacacc ttgaatgaca atgctnggag cccccctgtg gtcacgcagc cctccactgc 60
cattgatgca ccatccaacc tgcgtttcct ggccaccaca cccaattcct tgctgggtac 120
atggcagccg ccacgtgcc a ggattaccgg ctacatcatc aagtatgaga agcctgggtc 180
tcctcccaga gaagtgggtc ctcggccccg cctggtgtgc acagaggcta ctattactgg 240
c                                                                 241
```

<210> 397

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 90

<223> n = A,T,C or G

<400> 397

```
ggcaggtacc agcaggggga tgtgtttctg gggaattgtg gctctggaag cttcacgggt 60
tcccagaatg tggaaaatat atctgtgcan gatagaaatc ctgcccagag gctgtttctg 120
tctcatttga gctctccttc atgtggcaga gctgactgtg gcggtttagg agcctacatt 180
ttagaaaagc ttacctcaaa gttctgcatt gagcctgagc actggaaagg agataaaata 240
a                                                                 241
```

<210> 398

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 3, 11, 22, 27, 38, 41, 53, 59, 63, 69, 77, 78, 94, 131, 133,  
137, 149, 154, 162, 166, 167, 172, 175, 176, 179, 191, 230

<223> n = A,T,C or G

&lt;400&gt; 398

```
gangtgacca ngacatcacc tnacacntgg aaagcganga nttgaatggt gcntacaang 60
ccntaccnt tgcccannac ctgaacgcgc cttntgattg ggacagccgt ggggaaggaca 120
gttatgaaac nantcanctg gatgaccana gtgntgaaac cnacanncac angcnntcna 180
cattatataa ncggaagct aatgatgaga gcaatgatca ttccgatgtn attgatagtc 240
a                                                                 241
```

&lt;210&gt; 399

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 212, 226

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 399

```
cagagtgaga tgggagtggg agggccaatc tgatacagaa gggggtgaag ggtagggccc 60
ctgagcagcc cacccttac cctgacgaag gcaatcctcc tctggaatgt ctcttccctc 120
ttcagctctg gtctctgcctc agccacgaac tgggaaggag tgaggaacat cccaacggca 180
atgagagtat ccagtgact ccaaacagga angaatcagt gttcanaaag tcagggccct 240
t                                                                 241
```

&lt;210&gt; 400

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 400

```
ggtactcttg ctcttttagc tagagtgtat gtgaaaataa agaaatacat cattgtattc 60
acaaccatgt gtcttcattt ataacttttt gtttaaaaaa tttttagttc aagtttagtt 120
cattgatatt atcctctgaa tgcagttaag gctgggcaga aattctactc atgtgacatc 180
tgccacaggt ctattttgaa gcttttcttc taatgggcaa tgtttgtcct taccaggatt 240
t                                                                 241
```

&lt;210&gt; 401

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 1, 2

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 401

```
nncagggtact ttgtagagca gagagaggct ttgggttcctc ctttcttcaa tcacgtggag 60
atgtgtcatc acctgggatt tcatctgggc cgccttttct gggtcacacag ccaacacatg 120
ctggtaatga cggatggtat gtaagcgatc tttgttctca gcacggacat aacgccgtaa 180
ggcctggaga atgcgatgag gccgtggcgg gtcagactgc aaggcagcca ggtagttctc 240
c                                                                 241
```

&lt;210&gt; 402

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 26, 27  
 <223> n = A,T,C or G

<400> 402  
 ggcaggtcca aaaaaaacct aaaaanngtt tcaggaatgt agagaaatat ccaacttaaa 60  
 tagcgaaaaa gtgcaccata attactgctg cactgcagtc atttctgcaa ttcccatggt 120  
 tcttaaataa ctatcttgtc agataacaca caatataaag agcaattatg aaaaacagac 180  
 atttacatat acttctaaaag tcttattggg aatatcctgt ttggccattg ggataaccaa 240  
 t 241

<210> 403  
 <211> 241  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 49  
 <223> n = A,T,C or G

<400> 403  
 aggtgttaac taccgctcc gagacgggat tgatgacgag tcctatgang ccattttcaa 60  
 gccggtcatg tccaaagtaa tggagatggt ccagcctagt gcggtggtct tacagtgtgg 120  
 ctccagactcc ctatctgggg atcggttagg ttgcttcaat ctaactatca aaggacacgc 180  
 caagtgtgtg gaatttgtca agagctttaa cctgcctatg ctgatgctgg gaggcggtgg 240  
 t 241

<210> 404  
 <211> 241  
 <212> DNA  
 <213> Homo sapiens

<400> 404  
 caggtactgc aaccataaa atactgtttc ctcataattc accttcctta atttgagatt 60  
 ttctgtcttc ttttcacggc attcaaagta ggaataaact ttgcttgtgt tgggtggata 120  
 ttgtttatag tgagtaacct tgtaggagtc ggtggccagg aggatgttga actcggcttc 180  
 tgccgcagga ttcattctcg gccggaggac aaggggcccg cgcgccgcga gctccctgac 240  
 c 241

<210> 405  
 <211> 266  
 <212> DNA  
 <213> Homo sapiens

<400> 405  
 ttctgggctg gggagtggag agaaagaagt tgcagggtt acaggaaatc ccagagcctg 60  
 aggttttctc ccagatttga gaactctaga ttctgcatca ttatctttga gtctatattc 120  
 tcttgggctg taagaagatg aggaatgtaa taggtctgcc ccaagccttt catgccttct 180  
 gtaccaagct tgtttccttg tgcattcctc ccaggctctg gctgcccctt attggagaat 240  
 gtgatttcca agacaatcaa tccaca 266

<210> 406  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<400> 406  
ttggtgaaga accattcctc ggcattcctg cggttcttct ctgccatctt ctcatactgg 60  
tcacgcatct cgttcagaat gcggctcagg tccacgccag gtgcagcgtc catctccaca 120  
ttgacatctc caccacactg gcctctcagg gcattcatct cctcctcgtg gttcttcttc 180  
aggtaggcca gtcctcctt caggctctca atctgcatct ccaggtcagc t 231

<210> 407  
<211> 266  
<212> DNA  
<213> Homo sapiens

<400> 407  
cagcatcatt gtttataatc agaaactctg gtccttctgt ctggtggcac ttagagtctt 60  
ttgtgccata atgcagcagt atggaggagg gattttatgg agaaatgggg atagtcttca 120  
tgaccacaaa taaataaagg aaaactaagc tgcattgtgg gttttgaaaa gggtattata 180  
cttcttaaca attctttttt tcagggactt ttctagctgt atgactgtta cttgaccttc 240  
tttgaaaagc attcccaaaa tgcctc 266

<210> 408  
<211> 261  
<212> DNA  
<213> Homo sapiens

<400> 408  
ctgtgtcagc gagcctcggg acactgattt ccgatcaaaa gaatcatcat ctttaccttg 60  
acttttcagg gaattactga actttcttct cagaagatag ggacacagcca ttgccttggc 120  
ctcacttgaa gggctctgcat ttgggtcctc tggctctctg ccaagtcttc cagccactcg 180  
agggagtaat atctggaggg caaagaagag acttatgtta ttgttgaacc tccagccaca 240  
gggaggagca tgggcatggg t 261

<210> 409  
<211> 266  
<212> DNA  
<213> Homo sapiens

<400> 409  
gctgacagta atacactgcc acatcttcag cctgcaggct gctgatgggtg agagtgaat 60  
ctgtcccaga cccgctgcc aatgaatcgt cagggatccc ggattcccgg gtagatgccc 120  
agtaaagtga cagtttagga ggctgtcctg gttctctgct gtaccaagct aagtagttct 180  
tattgttgga gctgtctaaa acactctggc tggctcttga gttgatgggtg gccctctcgc 240  
ccagagacac agccaggag tgtgga 266

<210> 410  
<211> 181  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 9, 17, 24, 26, 65, 97, 98, 99, 100, 103, 105, 106, 107, 108,  
120, 121, 123, 142, 145, 149, 162, 177  
<223> n = A,T,C or G

<400> 410  
caaaaggtn tttttgntca aaancnattt ttattccttg atatttttct ttttttttt 60  
tttgnggatg gggacttggt aatttttcta aaggggnnnn ttnannnnngg aagaaaaccn 120  
ngntccggtt ccagccaaac cngtngctna ctttccacct tnttccacc tccctcnggt 180

t 181

<210> 411  
<211> 261  
<212> DNA  
<213> Homo sapiens

<400> 411  
gcccctgcag tacttggccg atgtggacac ctctgatgag gaaagcatcc gggctcacgt 60  
gatggcctcc caccattcca agcggagagg ccgggcgtct tctgagagtc agggctctag 120  
tgctggagtg cgcacggagg ccgatgtaga ggaggaggcc ctgaggagga agctggagga 180  
gctggccagc aacgtcagtg accaggagac ctctccgag gaggaggaag ccaaggacga 240  
aaaggcagag cccaacaggg a 261

<210> 412  
<211> 171  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 1, 6, 53, 79, 91, 96, 114, 132  
<223> n = A,T,C or G

<400> 412  
ntttntctt tacaattcag tcttcaacaa cttgagagct ttcttcatgt tgncaagcaa 60  
cagagctgta tctgcaggnt cgtaagcata nagacngttt gaatatcttc cagngatato 120  
ggctctaact gncagagatg ggtcaacaaa cataatcctg gggacatact g 171

<210> 413  
<211> 266  
<212> DNA  
<213> Homo sapiens

<400> 413  
ttaggaccaa agatagcatc aactgtatct gaaggaactg tagtttgccg attttatgac 60  
atttttataa agtactgtaa ttctttcatt gaggggctat gtgatggaga cagactaact 120  
cattttgtta ttgcatataa aattatcttg ggtctctgtt caaatgagtt tggagaatgc 180  
ttgacttggt ggtctgtgta aatgtgtata tatatatacc tgaatacagg aacatcggag 240  
acctattcac tcccacacac tctgct 266

<210> 414  
<211> 266  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 86, 153, 162, 178, 184, 205  
<223> n = A,T,C or G

<400> 414  
tttgccataa ttgagtgaag agtggcagat ggcattaact ctgctccgct tcaagctggc 60  
tccatgacca ctcaaggcct ccccancttg ttcgtcaagt tgcctcaag tccaagcaat 120  
ggaatccatg tgtttgcaaa aaaagtgtgc tanttttaag gncctttcgt taagaatnaa 180  
tganacaatt ttcctaccaa aggangaaca aaaggataaa tataatacaa aatatatgta 240  
tatgggtggt tgacaaatta tataac 266

<210> 415  
<211> 266  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 37, 103, 223  
<223> n = A,T,C or G

<400> 415  
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tggcttcatt cagctccggt tcccaacgat caaggcgagt tacatgatcc cccatgttgt 180  
gcaaaaaagc ggtagctcc ttcggtcctc cgatcgttgt canaagtaag ttggccgcag 240  
tgttatcact catggttatg gcagca 266

<210> 416  
<211> 878  
<212> DNA  
<213> Homo sapiens

<400> 416  
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aaaaagacgc ctcaaaattc actcaacttt tgagacagca atggcaatag gcagcagaga 180  
agctatgctg caactgaggg cacatatcat tgaagatgtc acaggagttt aagagacagg 240  
ctggaaaaaa tctcactact agcaaacagt agtatctcat accaagcaaa accaagtagt 300  
atctgctcag cctgccgcta acagatctca caatcaccaa ctgtgcttta ggactgtcac 360  
caaaagtcaga ttcggtgcta accaggtggc atctatgac aacgtcgccc ctcttattta 420  
acaaagggct ctgaaggagg tgttctccaa gcaacaagga gactgcttca gtacaagact 480  
ttgcaccttg aattcaattg catcaagtgt ggatagcaaa ataagtatct taccattgaa 540  
atatgtgttc agcctaagat tttaccacac agcagaacaa aagtgagggg gagagggatg 600  
ggccagttag gggatggggg agaaaaaaaa atcacaggat taccacaaa gccttggttt 660  
aaaagggtc ccttcactat tcaggaaggg aagtggagg agaaattaac caattcctgc 720  
cacagcagcc ctttttggtc gcttcacaaa tagatacttt atggagtggc acagccaacc 780  
ctatctgtga cctgccctgc ggataaacac agccaagcag gtttaattag atcaaagaca 840  
caaagggtca ttcctcctt tcataaacac gcagacct 878

<210> 417  
<211> 514  
<212> DNA  
<213> Homo sapiens

<400> 417  
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caccagcgg gagtgggat gtgagacagc ccacattgga aaatccagaa aaccgggaac 180  
agggatttgc ccttcacaat tctactcccc agatcctctc ccctggacac aggagacca 240  
cagggcagga ccctaagatc tggggaaagg agtcctgag aaccttgagg tacccttaga 300  
tccttttcta cccactttcc tatggaggat tccaagtcac cacttctctc accggcttct 360  
accaggggtcc aggactaagg cgttttctcc atagcctcaa cattttggga atcttccctt 420  
aatcacccctt gctcctctg ggtgcctgga agatggactg gcagagacct ctttggtgcg 480  
ttttgtgctt tgatgccagg aatgccgcct agtt 514

<210> 418  
<211> 352  
<212> DNA

<213> Homo sapiens

<400> 418

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ccagtagaac cagaatcaga caggtatgag ctagtcaaca gcaagtcttt gttggattcg 120
agtaggctca ggatctgctg aaggctggag gagttagtcc ccgcaatcaa gagcctgtct 180
tcctgaagcc cttgggtgata ttttgccact cagccaagaa tgaggatgca tccttcagat 240
tctctatgtc ccgaacctgg aacccatcca cgccagcttg cagccaaaac tccagagcat 300
ccttcacctt ggttgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 352
```

<210> 419

<211> 344

<212> DNA

<213> Homo sapiens

<400> 419

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attgagactc aaaggcttat actggcgtct gaaactatgt ccttcgttaa acccgtattt 180
tggtgattcg atgtaaaatg gagtctggcc tccctcaaag cccaagcggg gccgggttcc 240
tctttgcctt tctcctttat ggcctctgcc acattttcta cctctctctc gacctcttgg 300
tcttctctcc ggtttcttgg agccgggatt cggctttaag ttgg 344
```

<210> 420

<211> 935

<212> DNA

<213> Homo sapiens

<400> 420

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cgaggttctc aaagatccaa aggagggaaa gggatttga aacactgtgt atcatctgag 180
acacacgtgt cctcatgatc ttaaatgcct actttaaaag cacctaatac tgcccttcat 240
tgtggtcaga agagatttct acaaaagcac tcagaattct ggaggcagtt gtgattttgc 300
catgtggcag ttggtttgtg gagttgggca ggtgtgaaag ggtaaaactc cacttctgaa 360
tgctgcttct gccccctggg acccagcaca ttgttagacc atcttcttga ctgaaaattc 420
tctcctgatg ctgagccctg caccaccacc ttccitttcc taactatgaa ttgatggcaa 480
agtcactca aaacaaccag ttaagtgtc acgagagagt agtcaagcac ctccagaaag 540
aaaccgggtt tttgttcaca tagcaggaag tgactccctg ggtggttaatt tatcttgaa 600
acacaggtag attggcagaa aaacgggaac atgtaggtag cgcatgttg gtgcatgtcc 660
attacttttg gatagcttt ctcagtcctt cctcaaata tagttgagcc agttttccag 720
tggaattct gagtgacttg cgcttgcctt atggtgtggt caaggagcgt tcagaactac 780
ggaaaacttt tactgaaaca gcgaagcaga gtataccggc atgagagggg agatgaacac 840
tcacctatgt accactcttt gacaataaat atagtatttc tcaaaaaaaaa aaaaaaaaaa 900
agtaaaaaaa ctgaaatcgc aagtcaaaaa atcca 935
```

<210> 421

<211> 745

<212> DNA

<213> Homo sapiens

<400> 421

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ggttaacaac agtcccctgc ttggcttcta ttctgaatcc ttttctttca ccatgggggtg 180
cctgaagggt ggctgatgca tatggtacaa tggcaccag tgtaaaagcag ctacaattag 240
gagtggatgt gttctgtagc atcctattta aataagccta ttttatcctt tggcccgctca 300
actctgttat ctgctgcttg tactgggtgcc tgtacttttc tgactctcat tgaccatatt 360
```

```
ccacgaccat ggttgatc cttacttga tctacttta catgtctagt ctgtgtggtt 420
ggtggtgaat aggtctcttt ttacatggtg ctgccagccc agctaattaa tgggtgcacgt 480
ggacttttag caagcgggct cactggaaga gactgaacct ggcattggaat tcctgaagat 540
gtttgggggt tttttcttct ttaatcgaaa gttaacattg tctgaaaagt tttgttagaa 600
ctactgcgga acctcaaaat cagtagattt ggaagtgtt caaagctaaa ctttttcctt 660
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tttgcttctt tgttagttgt cagac 745
```

&lt;210&gt; 422

&lt;211&gt; 764

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 422

```
gagttcagta gcaaagtcac acctgtccaa ttccctgagc tttgctcact cagctaattg 60
gatggcaaa ggtgtggtgc ttcatcttc aggcagaagc ctctgcccac cccctcaag 120
ggctgcaggc ccagttctca tgctgccctt ggtgggcat ctgttaacag aggagaacgt 180
ctgggtggcg gcagcagctt tgcctgagt gcctacaaag ctaatgcttg gtgctagaaa 240
catcatcatt attaaacttc agaaaagcag cagccatggt cagtcaggct catgctgcct 300
cactgcttaa gtgcctgcag gagccgcctg ccaagctccc ctctctacac ctggcacact 360
ggggtctgca caaggtttg tcaaccaaag acagcttccc ccttttgatt gcctgtagac 420
tttgagacca agaaacactc tgtgtgactc tacacacact tcagggtggt tgtgcttcaa 480
agtcattgat gcaacttgaa aggaaacagt ttaatggtg aaatgaaacta ccatttataa 540
cttctgtttt ttattgaga aaatgattca cgaattccaa atcagattgc caggaagaaa 600
taggacgtga cggtagctgg ccctgtgatt ctcccagccc ttgcagtcct ctaggtgaga 660
ggaaaagctc tttacttccg cccctggcag ggacttcttg gttatgggag aaaccagaga 720
tgggaatgag gaaaatatga actacagcag aagcccctgg gcag 764
```

&lt;210&gt; 423

&lt;211&gt; 1041

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 423

```
ctcagagagg ttgaaagatt tgccacgaa agggacagt atgaagctaa gctctagatc 60
caggatgtct gacttcaaat tgaaactccc aaagtaatga gtttggaagg gtggggtgtg 120
gcctttccag gatgggggtc ttttctgctc ccagcggata gtgaaacccc tgtctgcacc 180
tggttggcg tggtgctttc ccaaaggttt ttttttagg tccgtcgtc tcttggtgat 240
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agctcagggc cacagtgcga tgaggacat ctctcacct ctctaaatgc aggaagaaac 360
gcagagtaac gtggaagtgg tccacaccta ccgccagcac attgtgaatg acatgaaccc 420
cggcaacctg cacctgttca tcaatgccta caacaggtat tgggatgtag ttcagccaca 480
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gtccccagga aggacacctg gcctgtaagc tggttcctgg cattcagctc gccttgacag 660
gatctgaaca aacctccag accactgggg gtgcagacgt gagagggacg cagtcgcaca 720
ctcagagggt tgagagtaaa tatgtgtgcc cgtgctgac ctacacgaaa ggccaaatgt 780
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tcagggccat tgggtgcagc cagagactct gtaatcttcc agggagctcg ctcaacctgc 1020
tgagctcgtc ctgccacgca c 1041
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&lt;210&gt; 424

&lt;211&gt; 1288

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 424

```

ctaagaactg agacttgtga cacaaggcca acgacctaa attagcccag ggttgtagct 60
ggaagaccta caacccaagg atggaaggcc cctgtcaca agcctaccta gatggataga 120
ggacccaagc gaaaaaggta tctcaagact aacggccgga atctggaggc ccatgaccca 180
gaacccagga aggatagaag cttgaagacc tggggaaatc ccaagatgag aacctaaac 240
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ccaaaatcca gtcagtatct aatctggctt ttgttaactt ccctcaggag cagacattca 540
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agaagcacct gccagcaaca gcttccttct ttgagcttag tccatccctc atgaaaaatg 780
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cttaagccat ctagatgtca caattgaaac aaactgggga gttggttgct attgtaaaa 1260
aaaatatact gttttgaaaa aaaaaaac

```

&lt;210&gt; 425

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 425

```

ccacttaaa ggtgcctctg ccaactggtg gaatcatcgc cacttccagc accacgccaa 60
gcctaacatc ttccacaagg atcccgatgt gaacatgctg cacgtgtttg ttctgggcga 120
atggcagccc atcgagtacg gcaagaagaa gctgaaatac ctgccctaca atcaccagca 180
cgaataactc ttcttgattg ggccgccgct gctcatcccc atgtatttcc agtaccagat 240
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catccggttc ttcatcacct acatcccttt ctacggcatc ctgggagccc tccttttctt 360
caacttcac aggttccttg agagccactg gtttgtgtgg gtcacacaga tgaatcacat 420
cgtcatggag attgaccagg aggacc

```

&lt;210&gt; 426

&lt;211&gt; 874

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 426

```

tttttttttt tttttttttt ttttttcaat taaagatttg atttattcaa gtatgtgaaa 60
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tacagccatg ctgtttcaga agacttgaaa tgccattgat agtttaaaaa ctctacacc 180
gatggagaat cgaggaagac aatttaaatg ttcatctgaa tccagaggtg catcaaatta 240
aatgacagct ccacttggca aataaatagct gttacttgat ggtatccaag aagaaatgg 300
tggtgatgga taaattcaga aatgcttccc caaaggtggg tggtttttaa aaagttttca 360
ggtcacacac cttgcagaaa acactgatgc ccaacacact gattgcgggt ccaggaaaca 420
cgggtcttcc aagttccaag gggctggggg tccccaacga tcaagttcct gtgctgta 480
caagaggggc ctttgactg gatagggagc acttgggagc tgtacaccat cagtcataat 540
ggatggcagtg gtaaaagatg atccaaatga cctgagatgc tcctgaggag tgggtgcacca 600
gacccaggag tgccactgta gggctgcttc tttgctttag tcatcacaca cacacacagc 660
tccagagcag caatggcctt tcctgtaaca ggaaaaaagc ctctgtctat tcccaagaac 720
cctcgtaatg gcaaaactcc ccaaagtaca cccaggacca cagcaatgat ctgtcggaa 780

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 ttactccaga cggagacttt gagggccccc ttgg 874

<210> 427

<211> 638

<212> DNA

<213> Homo sapiens

<400> 427

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 aaaaatgata gtgattttga tgtaatttat ctcttggttg aatctgtcat tcaaaggcca 180  
 ataatttaag ttgctatcag ctgatattag tagctttgca accctgatag agtaaatataa 240  
 ttttatgggc ggggtgcaaaa tactgctgtg aatctatttg tatagtatcc atgaatgaat 300  
 ttatggaaat agatatattgt gcagctcaat ttatgcagag attaaatgac atcataatac 360  
 tggatgaaaa ctgtcataga attctgatta aatagtggtt ctgtttcaca tgtgcagttt 420  
 gaagtattta aataaccact cctttcacag tttattttct tctcaagcgt ttccaagatc 480  
 tagcatgtgg attttaaaaag atttgccctc attaacaaga ataacattta aaggagattg 540  
 tttcaaaata tttttgcaaa ttgagataag gacagaaaga ttgagaaaca ttgtatatatt 600  
 tgcaaaaaca agatgtttgt agctgtttca gagagagt 638

<210> 428

<211> 535

<212> DNA

<213> Homo sapiens

<400> 428

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 atcttgcaag taaggaaagg atgggtcattg ccttggtgga tggctcgagga acagctttcc 180  
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 acacagagag attcatgggt ctcccaacaa aggatgataa tcttgagcac tataagaatt 480  
 caactgtgat ggcaagagca gaatatattca gaaatgtaga ctatcttctc atcca 535

<210> 429

<211> 675

<212> DNA

<213> Homo sapiens

<400> 429

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 aaatacatag ttttcaataa ataatgtta attttacaac tttgatacag caatgtcata 180  
 caccgtttca acacactaca ctctgcatgc tagatagtct acgagaagac gaaactttgc 240  
 catgcatatt ctttcccccc tagtgctatc aaacacttca tctccagcg cactgcctca 300  
 ggtagcttta ccttctctct gtttcacagc aataggccgt gcgctggcat gcaaactcta 360  
 aaaaaggtcc ccccccacaa ccaactcagac ttctacacaa aagggttttt cagcttttct 420  
 gctcccaaac ctggagtggc taagaaagta agtttcatgt ggccttgga aatacacact 480  
 tgtaaacagt gtcattgtga aaactgctct aaaacatcag gtggttctgt cctgggtggc 540  
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 tccgttttaa aacagtcaat tcaaaaaagg tgtcacagaa caaatgcaaa agactcttaa 660  
 acccacaaca tatgt 675

<210> 430

<211> 434

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 430

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acctctgcc  gaagtccagc  gagaggacct  cacagtagag  cacaggccac  tccgggagtg  60
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gagccacctt  gtccattgcc  agggacttgg  tgggtgcagg  ctgtgttact  cctgagagct  180
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gattgtcata  ctcatagcct  tgggctgaaa  cgacctctcc  atttacaagg  agccggaggg  300
cacctgggac  agtcattctca  aagtcgggtc  ctacgaggct  gctgagatac  tccttgtgcc  360
ggccataaag  atccttgaac  actcgccgtt  cccgctcctc  ctctccggc  tgtgcgtggg  420
gggaaacatt  gtcg                                     434

```

&lt;210&gt; 431

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 431

```

acacaagcct  ccagcccgac  ccagcggcct  aatgaaactc  tggcaacctc  tcctgggcgt  60
ggccacgagt  atccagctcc  aagcccaagt  gaggcgggga  gtcaacttcc  ccatgattgc  120
caagtgaacca  agaccagaag  cagggacgat  taggctagtt  ctgaggcaag  gtgaactgga  180
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tgcctttgca  aggacctgct  ctgtccactc  caaatcaaag  gatacttgca  tccttcttac  300
acagactccc  atctctctgc  tcatagtgg  cccaggctgc  ccgagaaaaa  gaaacttggg  360
tcagtagaag  gctcattagt  gtgaaggagt  gagaggccag  gccttcctgt  gacataatgc  420
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caagcaccac  tggatggctc  tggagccagg  ggacttctat  gcacatacaa  ccaacatcac  540
cccactctgc  tcattctgtc  ctccaccctg  aacagcagag  t                                     581

```

&lt;210&gt; 432

&lt;211&gt; 532

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 432

```

actccaactc  aagttttacaa  gttacacctt  tgccacagcc  ttggctaaat  cttgaactag  60
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cttgacagtc  atgtgttttg  taagtccttg  atttaccatg  actacattct  tagccagggtg  180
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ccattcacca  ttatccagaa  ttttcagtgc  taagcaaaaa  gctcctgctg  caatttgaga  300
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agtatgttg  tcgacatcaa  cctctccaat  cttagatgct  ctccgaagga  agtgcaaagg  420
tagaggccga  cccagaccaa  agtttaaagc  tcttagaatc  ttcatttcca  tctgtctgat  480
ttggtgctta  gtataagtgt  tgtcagtcac  aaaagcaag  tcaccaattt  ct                                     532

```

&lt;210&gt; 433

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 433

```

acttggtttt  acagctcctt  tgaaaactct  gtgtttggaa  tatctctaaa  aacatagaaa  60
acactacagt  ggttttagaaa  ttactaat  tacttctaag  tcattcataa  accttgtcta  120
tgaaatgact  tcttaaata  ttagttgata  gactgtaca  ggtaatagg  acttagcaag  180
ctcttttata  tgctaaagga  gcattctatca  gattaagtta  gaacatttgc  tgtcagccac  240
atattgagat  gacactaggt  gcaatagcag  ggatagattt  tgttggtag  tagtctcatg  300
ccttgagatc  tgtggtggtc  ttcaaaatgg  tggccagcca  gatcaaggat  gtagtatctc  360

```

atagttccca ggtgatattt ttcttattag aaaaatatta taactcattt gttgtttgac 420  
acttatagat tgaaatttcc taatttattc taaattttta gtggttcttt ggttccagt 480  
ctttatgttg ttgttgtttt tggatgtgtg tacatattat atgttctaga a 531

<210> 434

<211> 530

<212> DNA

<213> Homo sapiens

<400> 434

acaagagaaa acccctaaaa aaaggatggc tttagatgac aagctctacc agagagactt 60  
agaagttgca ctagctttat cagtgaagga acttccaaca gtcaccacta atgtgcagaa 120  
ctctcaagat aaaagcattg aaaaacatgg cagtagtaaa atagaaacaa tgaataagtc 180  
tcctcatatc tctaattgca gtgtagccag tgattattta gatttggata agattactgt 240  
ggaagatgat gttggtggtg ttcaaggga aagaaaagca gcactctaaag ctgcagcaca 300  
gcagaggaag attcttctgg aaggcagtga tggatgagtg gctaatagaca ctgaaccaga 360  
ctttgcacct ggtgaagatt ctgaggatga ttctgatttt tgtgagagtg aggataatga 420  
cgaagacttc tctatgagaa aaagtaaagt taaagaaatt aaaaagaaag aagtgaaggt 480  
aaaatcccca gtagaaaaga aagagaagaa atctaaatcc aaatgtaatg 530

<210> 435

<211> 677

<212> DNA

<213> Homo sapiens

<400> 435

accttatgat ctaattaata gatattagaa acagtagaaa gacaagttac acgtcaatgc 60  
ccaatgacta gagtcaacat taaagagttg taatttaagt aatccaaact gacatctaata 120  
tccaaaatca tttataaaat gtatttggct ttggaatcca caggacttca aacaagcaaa 180  
gtttcactgc agatagtcac aaagatgcag atacactgaa atacttaaga gccttattaa 240  
tgatttttgt tattttggat cttctgtttt ttcttatta tggctccgaag cctccttaata 300  
accaatttat cagacagaag catgtcatct tgttgttcaa gataatccag taaattttca 360  
gtccattcaa gtgccgcttt atggctaata cgcttctctg gattcagttc tgtttttcta 420  
ctcttactgg aaggcttttg ctcagcagcc ttggtctggt cctcagcact ttcactgtca 480  
gtcagcacct gacagcttga gtcactgtc cgagagtcga accactgatc aatattctca 540  
atgtcaacat gttcacattc ttctgtgttc tgtaaaactg ttgctaaatt agctgctaaa 600  
atggctcctt catcaatggt catacctgaa ttctcttcat tgccagggaa aagttttttc 660  
catgcttttg ttatggt 677

<210> 436

<211> 573

<212> DNA

<213> Homo sapiens

<400> 436

acctcttagg gtgggagaaa tggatgaagag ttgttcctac aacttgctaa cctagtggac 60  
agggtagtag attagcatca tccggataga tgtgaagagg acggctgttt ggataataat 120  
taaggataaa atttgccag ttgacagatt ctgtttccag cagtttttac agcaacagt 180  
gagtgttca gtattgtgtt cctgtaaatt taattttgat ccgcaatcat ttggtatata 240  
atgctgtttg aagttttgtc ctatttgaaa agtcttgtgt tgcaggggtg cagttaagat 300  
ctttgtgatg aggaatggga tgggctaatt ttttgccgtt ttcttggaaat tgggggcatg 360  
gcaaatacag taggtagtt tagttcttta cacagaacat gataaactac acctgttgat 420  
gtcaccgtct gtcaatgaat attatagaag gtatgaaggt gtaattacca taataacaaa 480  
acaccctgtc ttttagggctg acctttcgtc ctttgacctc ctcagcctcc attcccatct 540  
tcgctcagac tgcaagtatg tttgtattaa tgt 573

<210> 437

<211> 645

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 605

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 437

```
acaattggta tccatatctt gttgaaattg taatgggaaa acaatatatt tcaatctcta 60
tgtagatagt ggggttttgt ttccataata tattctttta gtttactgta tgagttttgc 120
aggactgcat aatagatcac cacaatcata acatcttagg accacagaca tttatgagat 180
catggcttct gtgggttaga agtatgctca tgtcttaact gggtcctctg ctgagctcta 240
tctggctgca atcaagggtg cagctgggct gaattttcat ttggaatctt gactgggaaa 300
gagctcgctt ccaagggtcat gaagtgtgct ggcaaaatgt atgtttttat gacagtatga 360
ctgaaatccc aagctatctc ctgactttta gctgggtaat ctcaggccct aaatgttgcc 420
tacagttcct agaggctggt cacagttcct agccatgtgg atttcctcaa catggctgct 480
tgcttcatca agtcagcaag aatagcctgt catatcagtg tatatcaggc tcaactcagga 540
taatttcctt actgatgagc caaacactaa ctgatttttag agcttaacta catctgcaaa 600
attcngttca ccagaggcaa gtcatatcca ggggaaggaga agtgt 645
```

&lt;210&gt; 438

&lt;211&gt; 485

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 438

```
acagaattga gagacaagat tgcttghtaat ggagatgctt ctagctctca gataatacat 60
atcttctgatg aaaatgaagg aaaagaaatg tgtgttctgc gaatgactcg agctagacgt 120
tcccaggtag aacagcagca gctcatcact gttgaaaagg ctttggcaat tctttctcag 180
cctacaccct cacttggtgt ggatcatgag cgattaaaaa atcttttgaa gactgttggt 240
aaaaaaagtc aaaactacaa catatttcag ttggaatatt tgtatgcagt aatcagccaa 300
tgtatttatc ggcatcgcaa ggaccatgat aaaacatcac ttattcagaa aatggagcaa 360
gaggtagaaa acttcagttg ttccagatga tgatgtcatg gtatcgagta ttctttatat 420
tcagttccta ttttaagtcatt ttttgtcatg tccgcctaatt tgatgtagta tgaaccctg 480
catct 485
```

&lt;210&gt; 439

&lt;211&gt; 533

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 439

```
acagcagttt cctcatccct gcagctgtgt ttgaacaggt catttaccat actgtcctcc 60
aggttcaaca gtatggctcc aaatgatgaa atttcattct gatcttctgg ctgaagacta 120
ttctgtttgt gtatgtccac cacagttact ttatcccttc atctgtggat gggcagaatg 180
aaacatatat ggaatgttc tgtgcaataa aaacagcagt ggtaacacag atgtaggctc 240
tgagtgtctc actggagact gaagtccaca gatatgcaac aaagcctttg tctccctgat 300
gtttttgcct cctgctggtc atgtgctttc acacatcaag agaggacatt taacatttga 360
gccacagtgt catttgctgt tgtctgatgg ttggttgcca gagaatttga actggagatg 420
aactttatta tccaggacgc tgagagtata acatgcatga cagagctttt agagcactgt 480
gatgtaacat gtcaagcaga aatagggagc atgtttacag ccattctatg aaa 533
```

&lt;210&gt; 440

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 440

```

catggggtag ggggggtcggg gattcattga attgtggttg gcaggagcaa gccctgctca 60
cactctcaca ctgcaccca gaattgtcaa agatacagat tgtaaaaatc tacgatccct 120
cagtctcact cacaaaaaat aaaatctcat gtccccaacg aaccagagt cagacgacag 180
ctggagcatt ggccgggaca gtcagaaagg agacaagtga aaacggtcag atggacacag 240
gcggaggaga aaagacagag ggagagagac catcgggaac aatcagaggg gccgagacga 300
tcagaaaagg gtcagcccga gacaggctga gccagagttt c 341

```

&lt;210&gt; 441

&lt;211&gt; 572

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 53, 84, 132, 138, 148

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 441

```

aagtttgggg ataatttatt atgcagcaag agataatata caggacttct canagcactt 60
aatatgttaa tataaatctc caanaaaaaa gatatacaat gaaacattcc tcttagttat 120
ctggccaagg anactttntt tttttganaa tattcttcaa aaagctgac taatgatatg 180
gctctggtcc tacaattcca tgtaacttct aaccttgatt ttatctcatg agcaaatcat 240
ttatcttcc agaacctcaa cttttccctt ttacaaagta gaaataaacc atctgccttt 300
acataaatca ttaatacagc cctggatggg cagattctga gctatttttg gctggggggg 360
gggaaatagc ctgtggaggt cctaaaaaga tctacggggc tcgagatggg tctctgcaag 420
gtagcaggtg ggctcagggc ccatttcagt ctttgttccc caggccattt ccacaaaatg 480
gtgagaaata gtgtcttctt ttagcttgct cataactcaa agatgggggg catggacctg 540
ggcctttcta ggctagggca tgaacctcct cc 572

```

&lt;210&gt; 442

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 34, 67

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 442

```

tcccagctgc actgcttaca cgtcttcctt cgtnttcacc taccocgagg ctgactcctt 60
ccccagntgt gcagctgccc accgcaaggg cagcagcagc aatgagcctt cctctgactc 120
gctcagctca cccacgtgc tggccctgtg agggggcagg gaaggggagg cagccggcac 180
ccacaagtgc cactgccga gctgggtgcat tacagagagg agaaacacat cttccctaga 240
gggttcctgt agacctaggg aggaccttat ctgtgcgtga aacacaccag gctgtggggc 300
tcaaggactt gaaagcatcc atgtgtggac tcaagtccctt acctcttccg gagatgtagc 360
aaaacgcatg gagtgtgta 379

```

&lt;210&gt; 443

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 444

&lt;223&gt; n = A,T,C or G

```

<400> 443
acatgcccc aaaggctcgc ttcattgcta cgattctcta cttaaatecca cattcacagc 60
tattgcctca gacctctcgg aggaggggcc aggggttagc tggctttgaa tagcatgtag 120
agcacaggca gtgtggccac aaatgtcaca caggtgacca ggggtctata gatgggtgtc 180
ctgttgactt gggcttctag tctctgctcc gtgtctgaca gtgccaagat catgctcccc 240
tgctccagca agaagctggg catagccccg tctgctgggt ccaccaggcc tgggtgtgct 300
gcgacttta caagctgaac caccacagcc atttggttac aagtcttttc taggccatca 360
agctgctctc gtaagccttc tagacatgaa tggacttgcc tggaatgact aagctgctct 420
ttcaaggcag ctgaaaggac atcnacatct ctgtctctgg tcgggggact acctgcctgt 480
gaccacagat cctgccctgg cccagcagca t
511

```

```

<210> 444
<211> 612
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 547
<223> n = A,T,C or G

```

```

<400> 444
acaggaagaa ttctacagtt aatctatcac agtgttccag caaagcatat gttgaaaact 60
acagttttta atctaacatc taaattttaa aaagtagcat ttcagcaaca aacaagctca 120
gagaggctca tggcaaaaagt gaaataacag aactattgct cagatgtctg caaagtcaag 180
ctgctgccct cagctccgcc cacttgaagg cttaggcaga cacgtaaggt ggcgggtggct 240
ccttggcagc accattcaca gtggcatcat catacggagg tagcagcacc gtagtgtcat 300
tgctggtaac ataaaccagg acatcagagg agttcctacc attgatgtat cggtagcagt 360
tccaaacaca gctaatacaag taacccttaa aagtcaagat aatgctaata aacagaagaa 420
taataaggac caaacaggta ggattcactg acatgacatc atctctgtag ggaaaattag 480
gaggcagttg ccgtatgtat tcctgaatgg agtttgata aataagcaca gtgattgcaa 540
ccaacancct cagggcaaaag tcaaagatct ggtaacagaa gaatgggatg atccaggctg 600
cgcgttgctt gt
612

```

```

<210> 445
<211> 708
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 643, 676
<223> n = A,T,C or G

```

```

<400> 445
accatcctgt tccaacagag ccattgccta ttctctaaatt gaatctgact ggggtgtgccc 60
ctcctcgga cacaacagta gaccttaata gtggaacat cgatgtgcct cccaacatga 120
caagctgggc cagctttcat aatgggtgtg ctgctggcct gaagatagct cctgcctccc 180
agatcgactc agcttgatt gtttacaata agccaagca tgctgagttg gccaatgagt 240
atgctggctt tctcatggct ctgggtttga atgggcacct taccagctg ggcactctca 300
atatccatga ctacttgacc aagggccatg aaatgacaag cattggactg ctacttggtg 360
tttctgctgc aaaactaggc accatggata tgtctattac tcggcttgtt agcattcgca 420
ttcctgctct cttaccccca acgtccacag agttggatgt tcctcacaat gtccaagtgg 480
ctgcagtggt tggcattggc cttgtatatc aagggacagc tcacagacat actgcagaag 540
tcctgttggc tgagatagga cggcctcctg gtctgaaat ggaatactgc actgacagag 600
agtcatactc cttagctgct ggcttgccc tgggcatggt ctncctgggg catggcagca 660
atttgatagg tatgtntgat ctcaatgtgc ctgagcagct ctatcagt
708

```

<210> 446  
<211> 612  
<212> DNA  
<213> Homo sapiens

<400> 446  
acaagcaacg cgcagcctgg atcatcccat tcttctgtta ccagatcttt gactttgccc 60  
tgaacatggt ggttgcaatc actgtgctta tttatccaaa ctccattcag gaatacatac 120  
ggcaactgcc tcctaatttt ccctacagag atgatgtcat gtcagtgaat cctacctgtt 180  
tggtccttat tattcttctg tttattagca ttatcttgac ttttaagggt tacttgatta 240  
gctgtgtttg gaactgctac cgatacatca atggtaggaa ctctctgat gtcctgggtt 300  
atgttaccag caatgacact acggtgctgc taccctcgta tgatgatgcc actgtgaatg 360  
gtgctgccaa ggagccaccg ccaccttacg tgtctgccta agccttcaag tgggcggagc 420  
tgagggcagc agcttgactt tgcagacatc tgagcaatag ttctgttatt tcaacttttc 480  
catgagcctc tctgagcttg tttgttgctg aaatgtact ttttaaaatt tagatgttag 540  
attgaaaact gtagttttca acatatgctt tgctggaaca ctgtgataga ttaactgtag 600  
aattcttcct gt 612

<210> 447  
<211> 642  
<212> DNA  
<213> Homo sapiens

<400> 447  
actgaaagaa ttaaagtcag aagtcttccc aaaacaaaaa gaactgccc aagagaaaat 60  
cctttctgat acttttcatt gctaaaataa aacaggcggg aaatgtggaa aagaaattca 120  
acaaaataat gtagcaccag aagaacaagt cctagatgat tcaagttcaa aaggtaagct 180  
ccagcaatgt ggaagaggta aagaccaatg tagacaagct gacgaggaat atcttctttt 240  
ttggttttct ggaagtagag ttcaggaaaa gcatgaagcc agtaagccag ctgtgatatg 300  
tagaaaaact tcatttgaaa tgtcatcagg ttatggggat aagccctcca taagatagtt 360  
gggtctgaga ttagtctttc agagatgaga atgaatgtgc cccaaacaca ggcaaaaagg 420  
tagaacgcac taagctgacc agattcatta aacttgctgt gttttgtttt ggagaagtgc 480  
attcgctgt taattttatc caacatatac ttttgaatta cggcatgaat aattatcgcc 540  
actagcatgt agaagaaaac agtagccaaa tctttgatgc catagtaata aagggacact 600  
gattcagtag cttgttcttc tgttgctggg agggtgacat tg 642

<210> 448  
<211> 394  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 66  
<223> n = A,T,C or G

<400> 448  
accagaagac cttagaaaaa ggaggaaagg aggagaggca gataatttgg atgaattcct 60  
caaagngttt gaaaatccag aggttcctag agaggaccag caacagcagc atcagcagcg 120  
tgatgttatc gatgagccca ttattgaaga gccaaagccg ctccaggagt cagtgatgga 180  
ggccagcaga acaaacatag atgagtcagc tatgctcca ccaccacctc agggaggtta 240  
gcgaaaaagct ggacaaattg acccagagcc tgtgatgcct cctcagcagg tagagcagat 300  
ggaaatacca cctgtagagc ttccccaga agaacctcca aatatctgtc agctaatacc 360  
agagtttagaa cttctgccag aaaaagagaa ggag 394

<210> 449  
<211> 494

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 66  
<223> n = A,T,C or G

<400> 449  
acaaaaaaca caaggaatac aaccaaatag aaaatagtcc tgggaatgtg gtcagaagca 60  
aaggcntgag tgtctttctc aaccgtgcaa aagccgtgtt cttcccggga aaccaggaaa 120  
aggatccgct actcaaaaac caagaattta aaggagtttc ttaaatttcg accttgtttc 180  
tgaagctcac ttttcagtgc cattgatgtg agatgtgctg gagtggctat taaccttttt 240  
ttcctaaaga ttattgttaa atagatattg tggtttgggg aagtigaatt ttttataggt 300  
taaattgcac tttagagatg gggagaggga ttatactgca ggcagcttca gccatgttgt 360  
gaaactgata aaagcaactt agcaaggcct cttttcatta ttttttatgt ttcaactata 420  
aagtcttagg taactagtag gatagaaaca ctgtgtcccg agagtaagga gagaagctac 480  
tattgattag agcc 494

<210> 450  
<211> 547  
<212> DNA  
<213> Homo sapiens

<400> 450  
acttttgggt ccagacttca ctgtccttag gcattgaaac catcacctgg tttgcattct 60  
tcatgactga ggtaaactta aaacaaaaat ggtaggaaag ctttcctatg cttcgggtaa 120  
gagacaaatt tgcttttgta gaattggtgg ctgagaaagg cagacagggc ctgattaaag 180  
aagacatttg tcaccactag ccaccaagtt aagtgtgga acccaaaggt gacggccatg 240  
gaaacgtaga tcatcagctc tgctaagtag ttagggggaag aaacatattc aaaccagtct 300  
ccaaatggga tcctgtggtt acagtgaatg gccactcctg ctttattttt cctgagattg 360  
ccgagaataa catggcactt atactgatgg gcagatgacc agatgaacat catcatccca 420  
agaatatgga accaccgtgc ttgcatcaat agatttttcc ctgttatgta ggcattcctg 480  
ccatccattg gcacttggtc cagcacagtt aggccaacaa ggacataata gacaagtcca 540  
aaacagt 547

<210> 451  
<211> 384  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 8, 9, 19, 41  
<223> n = A,T,C or G

<400> 451  
actacttntt ggtaaang ccactggtag agtcatctga ntgtaaacaa tgtccctgca 60  
ctgtgggaaa aatccactgg ctcccaagaa aagaaaatgg tctgaagcct ctgttggtggc 120  
tctcacaact catctttccc taagtcatca agctccacat cactgaggtc aatgtcatcc 180  
tccacgggaa gctcgccatc cctgccgtcc caaggctctc totcaacgat ggtagggaaa 240  
gccccgcctc ctacaggtgc cgtggagcca cgcccaaaag agagctccct gagaaactcg 300  
ttgatgcctt gctcactgaa ggagcctttt agcagagcaa atttcatctt gcgtgcattg 360  
atggcggcca tggcgggta ccca 384

<210> 452  
<211> 381  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 291, 341, 368

<223> n = A,T,C or G

<400> 452

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actctaaagt tgccactctc acaggggtca gtgataccca ctgaacctgg caggaacagt 60
cctgcagcca gaatctgcaa gcagcgcctg tatgcaacgt ttagggccaa aggctgtctg 120
gtgggggttg tcatcacagc ataatggcct agtaggtcaa ggatccaggg tgtgaggggc 180
tcaaagccag gaaaacgaat cctcaagtcc ttcagtagtc tgatgagaac tttaactgtg 240
gactgagaag ctttttcctc gaaccagcgg gcattgtcga tggctgctaa ngcactctgc 300
aatactttga tatccaaatg gagttctgga tccagttttc naagattggg tggcactgtt 360
gtaatganaa tcttcactgt a                                     381
```

<210> 453

<211> 455

<212> DNA

<213> Homo sapiens

<400> 453

```
actgtgctaa acagcctata gccaaagttt aaagagttac aggaacaact gctacacatt 60
caaagaacag gcattcactg cagcctcctg atttgacctg atgggagggg caggagaatg 120
agtcactctg ccaccacttt tcctgccttg gatttgtaga ggatttgttt tgctctaatt 180
tgtttttcct atatctgccc tactaaggta cacagtctgg gcactttgaa aatgttaaaag 240
tttttaacgt ttgactgaca gaagcagcac tttaaaggctt catgaatcta ttttccaaaa 300
aaagtatgct ttcagtaaaa cattttacca ttttatctaa ctatgcactg acatttttgt 360
tcttcctgaa aaggggatgt atgctaacac tgtattttta atgtaaaaat atacgtgtag 420
agatatatta acttcctgag tgacttatac ctcaa                                     455
```

<210> 454

<211> 383

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 9

<223> n = A,T,C or G

<400> 454

```
acagagcanc tttacaagtt gtcacatttc tttataaatt tttttaaaagc tacagttaa 60
tacaaaatga attgcggttt tattacatta ataacctttc acctcagggg tttatgaaga 120
ggaaaggggt ttatgcaaaa gaaagtgcta caattcctaa tcattttaga cacttttagga 180
gggggtgaag ttgtatgata aagcagatat ttttaattatt tggtatcttt ttgtattgca 240
agaaatttct tgctagttaa tcaagaaaac atccagattg acagtctaaa atggctactg 300
gtattttagt taattcaaaa atgaaacttt tcagtgtattc actttactaa cattctattt 360
gagaaggctt attggtaaag ttt                                     383
```

<210> 455

<211> 383

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 10

<223> n = A,T,C or G

<400> 455  
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 gtgcaggagc tgacttcttc caaagagttg tggttccggg cagcgggcat tgccgtgccc 120  
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 cacggacacc attccaaaaa ggggcaggtt gcaaagttag acttggaatg catgggtgccg 300  
 gtcagtgggc acgagaactg ctgtctgacc tgtgataaaa tgagacaagc agacctcagc 360  
 aacgataaga tcctctcgct tgt 383

<210> 456

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 64

<223> n = A,T,C or G

<400> 456  
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 cagctgaaac aggcctcttt cccagtgcac agcatatgtg gtcagtaata caaacgatgg 180  
 taaatgaggg tactacatag gccaggttaa caaactcctc ttctcctcgg gtaggccatg 240  
 atacaagtgg aactcatcaa ataattttaa cccaaggcga taacaacact atttcccatc 300  
 taaactcatt taagccttca caatgtcgca atggattcag ttacttgcaa acgatcccg 360  
 gttgtcatac agatacttgt tttttacaca taacgctgtg ccatcccttc cttcactgcc 420  
 ccagtcaggt ttctgttgtg tggaccgaaa ggggatacat tttagaaatg cttccctcaa 480  
 gacagaagtg agaaagaaag gagaccctga ggccaggatc tattaacacct ggtgtgtg 540  
 caa 543

<210> 457

<211> 544

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 17

<223> n = A,T,C or G

<400> 457  
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 gcccatgtca cattagggag agtgacaaa ccttcccttt tggcagaggg ttggactgag 120  
 gatagagcaa caatgaaatc attcagttca atgcacagtc cttgcatctg ctccctctgag 180  
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 ggatttttct tctgtgttgc ctgtagcttc attaagactc tattgactgc acacattgct 360  
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 tgacagaaat caaaagcttg aggaagcctc agttttctgc acaatgtttg aagtattctt 480  
 tccctggatg cttcatctgg gatacctagg catatttctc ggctgaacct tcccgcacgt 540  
 ctca 544

<210> 458

<211> 382

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 5, 23

<223> n = A,T,C or G

<400> 458

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cagaggagaa aactaaataa gtagagaaag ttttaactg cagaaattgg agtggatggg 240
ttctgcctta aattgggagg actccaagcc gggaaggaaa attccctttt ccaacctgta 300
tcaattttta caactttttt cctgaaagca gtttagtcca tactttgcac tgacatactt 360
tttccttctg tgctaaggta ag                                     382
```

<210> 459

<211> 168

<212> DNA

<213> Homo sapiens

<400> 459

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```

<210> 460

<211> 190

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 4

<223> n = A,T,C or G

<400> 460

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```

<210> 461

<211> 495

<212> DNA

<213> Homo sapiens

<400> 461

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ccaagaatg gtttacacca agcagagagg acatgtcact gaatggggaa aggggaacccc 180
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tccccactga cagag                                     495
```

<210> 462  
<211> 493  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 68  
<223> n = A,T,C or G

<400> 462  
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tctgccaagt gtgttttgga tacagagcac atcgtggctt ctggggtcac actcagctta 180  
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gagaaacaag aaggcaacat aataatgtta tcagaaagat gttaggaagt aaggacagct 360  
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ctgactctgc tga 493

<210> 463  
<211> 3681  
<212> DNA  
<213> Homo sapiens

<400> 463  
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tcgctctgtc actcaggctg g                                     3681

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&lt;210&gt; 464

&lt;211&gt; 1424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 464

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tgttggcaac agactatat gagagtgcg aaaaaggagct gaattattag tttgaattca 1380
agatattgca agacctgaga gaaaaaaaaa aaaaaaaaaa aaaa 1424

```

&lt;210&gt; 465

&lt;211&gt; 674

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 465

```

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cacaccctgg ggtaattaac ctggctcatcc ccaccctgga gagccatcct gcccatgggt 180
gatcaaagaa ggaacatctg caggaacacc tgatgaggct gcacccttgg cggaagaagc 240
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atttacgtgg ccagcaaaag gaagacctag gaagatcgca tgggagaaaa aagatgactc 540
agttaaggca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660
aaaaaaaaaa aaaa 674

```

&lt;210&gt; 466

&lt;211&gt; 1729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 11, 1128

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 466

```

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aagaagacac acctagggaa attatgagtc ccgcaaaaaga aacatctgag aaatttacgt 180
gggcagcaaa aggaagacct aggaagatcg catgggagaa aaaaagaaaca cctgtaaaga 240
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```

&lt;210&gt; 467

&lt;211&gt; 1337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

```

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tgaatcaggt ttctcacact catgaaaatg aaaattatct cttacatgaa aattgcatgt 1200
tgaaaaagga aattgccatg ctaaaactgg aaatagccac actgaaacac caataccagg 1260
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agatgacccc tcgtgcc 1337

```

&lt;210&gt; 468

&lt;211&gt; 2307

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 468

```

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tgaaatgcaa aagtctgttc caaataaagc cttggaattg aagaatgaac aaacattgag 720
agcagatcag atgttccctt cagaatcaaa acaaaagaac gttgaagaaa attcttgga 780
ttctgagagt ctccgtgaga ctgtttcaca gaaggatgtg tgtgtacca aggctacaca 840
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cttgatata gttcattctt gtgaaagagc aagggaactt caaaaagatc actgtgaaca 960
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agaagcaaaa gaaataaaat cacagttaga gaacccaaaa gttaaattggg aacaagagct 1080
ctgcagtgtg aggtttctca cactcatgaa aatgaaaatt atctcttaca tgaaaattgc 1140
atgttgaaaa aggaaattgc catgctaaaa ctggaaatag ccacactgaa acaccaatac 1200
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2307

```

&lt;210&gt; 469

&lt;211&gt; 650

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 310, 429, 522

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 469

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Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys
1      5      10      15
Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys
20     25     30
Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
35     40     45
Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
50     55     60
Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
65     70     75     80
Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
85     90     95
Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
100    105    110
Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
115    120    125
Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
130    135    140
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
145    150    155    160
Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
165    170    175

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Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His		
			180					185					190				
Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn		
		195					200					205					
Lys	Asp	Gly	Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro		
	210					215					220						
Thr	Lys	Ala	Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro		
225					230					235					240		
Pro	Gly	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser		
			245					250						255			
Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala		
			260					265					270				
Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser		
	275						280					285					
Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val		
	290					295				300							
Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly		
305					310					315					320		
Lys	Leu	Glu	Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys		
			325						330					335			
Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met		
			340					345					350				
Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro		
		355					360					365					
Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys		
	370					375					380						
Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys		
385					390					395					400		
Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu		
			405					410						415			
Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys		
			420					425					430				
Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp		
		435				440						445					
Gly	Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys		
	450					455					460						
Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu		
465					470					475					480		
Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro		
			485						490					495			
Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln		
			500					505					510				
Met	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Xaa	Val	Glu	Glu	Asn	Ser	Trp		
		515					520					525					
Asp	Ser	Glu	Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val		
	530					535					540						
Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu		
545					550					555					560		
Glu	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys		
			565						570					575			
Glu	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly		
			580					585					590				
Lys	Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu		
		595					600					605					
Ser	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys		
	610					615					620						
Trp	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Phe	Leu	Thr	Leu	Met	Lys	Met		
625					630					635					640		

Lys Ile Ile Ser Tyr Met Lys Ile Ala Cys  
645 650

<210> 470  
<211> 228  
<212> PRT  
<213> Homo sapiens

<400> 470  
Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys  
1 5 10 15  
Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys  
20 25 30  
Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu  
35 40 45  
Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr  
50 55 60  
Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu  
65 70 75 80  
Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser  
85 90 95  
Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met  
100 105 110  
Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe  
115 120 125  
Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu  
130 135 140  
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu  
145 150 155 160  
Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu  
165 170 175  
Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His  
180 185 190  
Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Lys Asn Arg  
195 200 205  
Phe Leu Phe Lys Asn Gln Leu Thr Glu Tyr Phe Ser Lys Leu Met Arg  
210 215 220  
Arg Asp Ile Leu  
225

<210> 471  
<211> 154  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> 148  
<223> Xaa = Any Amino Acid

<400> 471  
Met Arg Leu His Pro Trp Arg Lys Glu His Leu Thr Gln Leu Lys Ala  
1 5 10 15  
Trp Trp Lys Lys His Leu Met Arg Leu His Pro Trp Trp Lys Glu His  
20 25 30  
Leu Thr Arg Leu Lys Ala Trp Trp Lys Lys His Leu Met Arg Leu His

138

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      35      40      45
Pro Trp Trp Arg Glu His Leu Thr Lys Phe Asn Val Trp Arg Lys Arg
  50      55      60
His Leu Glu Ser Ser Asn Ser Gln Gln Lys Lys His Leu Gly Lys Leu
65      70      75      80
Arg Val Leu Gln Lys Lys His Leu Arg Asn Leu Arg Gly Gln Gln Lys
      85      90      95
Glu Asp Leu Gly Arg Ser His Gly Arg Lys Lys Met Thr Gln Leu Arg
      100      105      110
Gln Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
      115      120      125
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
      130      135      140
Lys Lys Lys Xaa Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
145      150

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&lt;210&gt; 472

&lt;211&gt; 466

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 329

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 472

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Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys
  1      5      10      15
Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys
      20      25      30
Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
      35      40      45
Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
      50      55      60
Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
65      70      75      80
Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
      85      90      95
Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
      100      105      110
Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
      115      120      125
Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
      130      135      140
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
145      150      155      160
Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
      165      170      175
Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His
      180      185      190
Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn
      195      200      205
Lys Asp Gly Leu Leu Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro
      210      215      220
Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro
225      230      235      240

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Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser
      245      250      255
Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala
      260      265      270
Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn
      275      280      285
Ser Trp Asp Thr Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val
      290      295      300
Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly
305      310      315      320
Lys Leu Glu Gly Ser Pro Gly Lys Xaa Gly Leu Leu Lys Ala Asn Cys
      325      330      335
Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met
      340      345      350
Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro
      355      360      365
Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys
      370      375      380
Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys
385      390      395      400
Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
      405      410      415
Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys
      420      425      430
Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Lys Asn Arg Phe Leu
      435      440      445
Phe Lys Asn His Leu Thr Lys Tyr Phe Ser Lys Leu Met Arg Lys Asp
      450      455      460
Ile Leu
465

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&lt;210&gt; 473

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 473

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Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys
1      5      10      15
Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr
      20      25      30
Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro
      35      40      45
Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val
      50      55      60
Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp
65      70      75      80
Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser
      85      90      95
Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys
      100      105      110
Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys
      115      120      125
Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ala Pro Cys Arg
      130      135      140
Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
145      150      155      160

```

Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala  
 165 170 175  
 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn  
 180 185 190  
 Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser Lys Gln  
 195 200 205  
 Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu Thr  
 210 215 220  
 Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln Lys Glu  
 225 230 235 240  
 Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser Lys  
 245 250 255  
 Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys  
 260 265 270  
 Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys Lys  
 275 280 285  
 Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser  
 290 295 300  
 Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val  
 305 310 315 320  
 Arg Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn Ala Asp Ile  
 325 330 335  
 Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His  
 340 345 350  
 Arg Lys Glu Leu Glu Val Lys Gln Leu Glu Gln Ala Leu Arg Ile  
 355 360 365  
 Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser  
 370 375 380  
 His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu  
 385 390 395 400  
 Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His  
 405 410 415  
 Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu  
 420 425 430  
 Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Pro Arg Ala  
 435 440 445

&lt;210&gt; 474

&lt;211&gt; 3865

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 474

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 ctgctgggcc ctgtgggcat ttattagtaa agttttaatg acaaaagctt tgagtcaaca 120  
 caccctgggg taattaacct ggtcatcccc accctggaga gccatcctgc ccatgggtga 180  
 tcaaagaagg aacatctgca ggaacacctg atgaggctgc acccttggcg gaaagaacac 240  
 ctgacacagc tgaagcttg gtgaaaaaa cacctgatga ggctgcaccc ttggtggaaa 300  
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 gaagacctag gaagatcgca tgggagaaaa aagaaacacc tgtaaagact ggatgcgtgg 660  
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 gtcctacaaa agaatacatc acaaaagcaa gtgccaatga tcagagggtc ccatcagaat 780  
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tcctgaagcc tacagacata aaataacagt gtgaagaatt acttgttcac gaattgcata 3780  
aagctgcaca ggattcccat ctaccctgat gatgcagcag acatcattca atccaaccag 3840  
aatctcgctc tgtcactcag gctgg 3865

&lt;210&gt; 475

&lt;211&gt; 1002

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 310, 429, 522

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 475

```

Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys
 1          5          10          15
Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys
          20          25          30
Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
          35          40          45
Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
          50          55          60
Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
          65          70          75          80
Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
          85          90          95
Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
          100          105          110
Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
          115          120          125
Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
          130          135          140
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
          145          150          155          160
Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
          165          170          175
Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His
          180          185          190
Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn
          195          200          205
Lys Asp Gly Leu Leu Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro
          210          215          220
Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro
          225          230          235          240
Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser
          245          250          255
Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala
          260          265          270
Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser
          275          280          285
Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val
          290          295          300
Cys Leu Pro Lys Ala Xaa His Gln Lys Glu Ile Asp Lys Ile Asn Gly
          305          310          315          320
Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys
          325          330          335
Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met
          340          345          350
Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro
          355          360          365
Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys
          370          375          380
Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys
          385          390          395          400
Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
          405          410          415
Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Xaa His Gln Lys

```

			420					425					430			
Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	
		435					440					445				
Gly	Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	
	450					455					460					
Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	
465					470					475					480	
Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	
				485					490					495		
Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	
			500					505					510			
Met	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Xaa	Val	Glu	Glu	Asn	Ser	Trp	
		515					520					525				
Asp	Ser	Glu	Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	
		530				535					540					
Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	
545					550					555					560	
Glu	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	
				565					570					575		
Glu	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	
			580					585					590			
Lys	Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	
		595					600					605				
Ser	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	
		610				615					620					
Trp	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu	
625					630				635						640	
Glu	Lys	Arg	Arg	Asn	Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile	Arg	Glu	Glu	
				645				650						655		
Leu	Gly	Arg	Ile	Glu	Glu	Gln	His	Arg	Lys	Glu	Leu	Glu	Val	Lys	Gln	
			660					665					670			
Gln	Leu	Glu	Gln	Ala	Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val	
		675					680					685				
Glu	Ser	Asn	Leu	Asn	Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr	
		690				695					700					
Leu	Leu	His	Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys	
705					710					715					720	
Leu	Glu	Ile	Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys	
				725					730					735		
Tyr	Phe	Glu	Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	Gln	
		740						745					750			
Met	Thr	Leu	Lys	Leu	Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln	
		755					760					765				
Tyr	Ser	Gly	Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr	
		770				775				</						

```
<210> 476
<211> 356
<212> DNA
<213> Homo sapiens
```

```
<400> 476
aggtctgccg gaaatgttag gcacccaac tcaagtcca ggccccaggc atctttctctg 60
ccctgccttg cttggcccat ccagtccagg cgctggagc aagtgtctag ctacttctcc 120
tgcactttga aagaccctc ccactcctgg cctcacattt ctctgtgtga tccccactt 180
ctgggctctg ccaccccaga gtgggaaagg ccaccctaga aagaagtccg ctggcaccca 240
taggaagggg cctcaggaga aggaagggcc aggcactaga ccttgccac ggcactgcc 300
ttctctgcct tcccttctct cctctgctct tgatctgtgt ttcaataaat taatgt 356
```

```
<210> 477
<211> 1876
<212> DNA
<213> Homo sapiens
```

<400>	477						
atgacctg	gctcaggatt	tgggtgggcgc	gccttcagct	gcattctcggc	ctgcggggccg	60	
cgccccggcc	gctgctgcat	caccgcgcgc	ccctaccgtg	gcattctcctg	ctaccgcgggc	120	
ctcaccgggg	gcttcggcag	ccacagcgtg	tgcggaggtg	ttcggggccgg	ctcctcgccga	180	
cgcagctctc	gtctaccgctc	cgggggcgtg	tgccggcccca	gtccccctag	catcaccacc	240	
gtgtcgggtca	acgagagcct	cctcacgccc	ctcaacctgg	agatcgaccc	caacgcgcag	300	
tgcgtgaagc	aggaggagaa	ggagcagatc	aagtcctcta	acagcaggtt	cgcggccttc	360	
atcgacaag	tgcgcttcct	ggagcagcag	aacaaactgc	tggagacaaa	gctgcagttc	420	
taccagaacc	cggagtgttg	ccagagcaac	ctggagcccc	tgtttgagtg	ctacatcgag	480	
actctcggcc	gggagtgctg	gtgcgtggag	gccgacagcg	ggaggctggc	ctcagagctt	540	
aaccacgtgc	aggaggtgct	ggagggtctc	aagaagaagt	atgaggagga	ggtttctctg	600	
agagcaaacg	ctgagaaagc	gttttctggct	ctgaagaagg	atgtggactg	cgcctacctc	660	
cgcaagtcat	acctggaggc	caactgggag	gccttgatcc	aggagatcga	cttctctagg	720	
cggctgtgat	aggaggagat	ccgattcttc	cagtcgcaca	ttctagacac	ctccgtggtt	780	
gtcaagctgg	acaacagccg	ggacctgaac	atggactgca	tcattgccga	gattaaggca	840	
cagtatgacg	acattgtcac	ccgcagcccg	gccgagcccg	agtcttggtc	ccgcagcaag	900	
tgtgaggagca	tgaaggccac	ggtgatcagg	cacggggaga	ccctgcgcgc	caccaaggag	960	
gagataaatg	agctgaaccg	catgatccaa	aggtctacgg	cgcagggtga	gaatgccaa	1020	
tgcagaactc	ccaagctgga	ggccgcggtg	gctcagttcg	acgagcaggg	tgaggcagcc	1080	
ctcagtgatg	cccgtgcaa	gctggccgag	ctggagggcg	ccctgcagaa	ggccaagcag	1140	
gacatggcct	gcctgatcac	ggagctaccg	gaggtgatga	actccaagct	gggcctggac	1200	
attcgagatc	ccacctatcg	gcgcctgtct	gagggcgagg	agcagaggct	atgtgaagct	1260	
attggggctg	tgaattctct	tgctcagcag	tccggggggc	gggtcgtgtg	cggggacctc	1320	

```

tgcgtgtcag gctcccggcc agtgactggc agtgtctgca gcgctccgtg caacgggaac 1380
gtggcgggtga gcaccggcct gtgtgcgccc tgcggccaat tgaacaccac ctgcggaggg 1440
ggttcctgcg gcgtgggctc ctgtgggtatc agctccctgg gtgtggggtc ttgcggcagc 1500
agctgccgga aatgttaggc accccaactc aagtcccagg ccccgagcat ctttcctgcc 1560
ctgccttgct tggcccatcc agtccaggcg cctggagcaa gtgtcagct acttctcctg 1620
cactttgaaa gaccctccc actcctggcc tcacatttct ctgtgtgatc cccacttct 1680
gggctctgcc accccacagt gggaaaggcc accctagaaa gaagtccgct ggcaccata 1740
ggaaggggcc tcaggagcag gaagggccag gaccagaacc ttgcccacgg caactgcctt 1800
cctgcctctc cccttcctcc tctgctcttg atctgtgttt caataaatta atgtagccaa 1860
aaaaaaaaa aaaaaa 1876

```

&lt;210&gt; 478

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 478

```

Met Thr Cys Gly Ser Gly Phe Gly Gly Arg Ala Phe Ser Cys Ile Ser
 1          5          10          15
Ala Cys Gly Pro Arg Pro Gly Arg Cys Cys Ile Thr Ala Ala Pro Tyr
 20          25          30
Arg Gly Ile Ser Cys Tyr Arg Gly Leu Thr Gly Gly Phe Gly Ser His
 35          40          45
Ser Val Cys Gly Gly Phe Arg Ala Gly Ser Cys Gly Arg Ser Phe Gly
 50          55          60
Tyr Arg Ser Gly Gly Val Cys Gly Pro Ser Pro Pro Cys Ile Thr Thr
 65          70          75          80
Val Ser Val Asn Glu Ser Leu Leu Thr Pro Leu Asn Leu Glu Ile Asp
 85          90          95
Pro Asn Ala Gln Cys Val Lys Gln Glu Glu Lys Glu Gln Ile Lys Ser
100          105          110
Leu Asn Ser Arg Phe Ala Ala Phe Ile Asp Lys Val Arg Phe Leu Glu
115          120          125
Gln Gln Asn Lys Leu Leu Glu Thr Lys Leu Gln Phe Tyr Gln Asn Arg
130          135          140
Glu Cys Cys Gln Ser Asn Leu Glu Pro Leu Phe Glu Gly Tyr Ile Glu
145          150          155          160
Thr Leu Arg Arg Glu Ala Glu Cys Val Glu Ala Asp Ser Gly Arg Leu
165          170          175
Ala Ser Glu Leu Asn His Val Gln Glu Val Leu Glu Gly Tyr Lys Lys
180          185          190
Lys Tyr Glu Glu Glu Val Ser Leu Arg Ala Thr Ala Glu Asn Glu Phe
195          200          205
Val Ala Leu Lys Lys Asp Val Asp Cys Ala Tyr Leu Arg Lys Ser Asp
210          215          220
Leu Glu Ala Asn Val Glu Ala Leu Ile Gln Glu Ile Asp Phe Leu Arg
225          230          235          240
Arg Leu Tyr Glu Glu Glu Ile Arg Ile Leu Gln Ser His Ile Ser Asp
245          250          255
Thr Ser Val Val Val Lys Leu Asp Asn Ser Arg Asp Leu Asn Met Asp
260          265          270
Cys Ile Ile Ala Glu Ile Lys Ala Gln Tyr Asp Asp Ile Val Thr Arg
275          280          285
Ser Arg Ala Glu Ala Glu Ser Trp Tyr Arg Ser Lys Cys Glu Glu Met
290          295          300
Lys Ala Thr Val Ile Arg His Gly Glu Thr Leu Arg Arg Thr Lys Glu
305          310          315          320
Glu Ile Asn Glu Leu Asn Arg Met Ile Gln Arg Leu Thr Ala Glu Val

```

```

          325          330          335
Glu Asn Ala Lys Cys Gln Asn Ser Lys Leu Glu Ala Ala Val Ala Gln
          340          345          350
Ser Glu Gln Gln Gly Glu Ala Ala Leu Ser Asp Ala Arg Cys Lys Leu
          355          360          365
Ala Glu Leu Glu Gly Ala Leu Gln Lys Ala Lys Gln Asp Met Ala Cys
          370          375          380
Leu Ile Arg Glu Tyr Gln Glu Val Met Asn Ser Lys Leu Gly Leu Asp
          385          390          395          400
Ile Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly Glu Glu Gln Arg
          405          410          415
Leu Cys Glu Gly Ile Gly Ala Val Asn Val Cys Val Ser Ser Ser Arg
          420          425          430
Gly Gly Val Val Cys Gly Asp Leu Cys Val Ser Gly Ser Arg Pro Val
          435          440          445
Thr Gly Ser Val Cys Ser Ala Pro Cys Asn Gly Asn Val Ala Val Ser
          450          455          460
Thr Gly Leu Cys Ala Pro Cys Gly Gln Leu Asn Thr Thr Cys Gly Gly
          465          470          475          480
Gly Ser Cys Gly Val Gly Ser Cys Gly Ile Ser Ser Leu Gly Val Gly
          485          490          495
Ser Cys Gly Ser Ser Cys Arg Lys Cys
          500          505

```

<210> 479  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 22  
 <223> n = A,T,C or G

```

<400> 479
ggtccattcc tttcctcgcg tnggggtttc tctgtgtcag cgagcctcgg tacactgatt 60
tccgatcaaa agaatcatca tctttacctt gacttttcag ggaattactg aactttcttc 120
tcagaagata gggcacagcc attgccttgg cctcacttga agggctctgca tttgggtcct 180
ctggtctctt gccaaagttc ccagccactc gagggagaaa t 221

```

<210> 480  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

```

<400> 480
cggcgaattc accatgggaa caagagctct gcagtg

```

36

<210> 481  
 <211> 62  
 <212> DNA  
 <213> Artificial Sequence

<220>

&lt;223&gt; PCR primer

&lt;400&gt; 481

cggcaagctt ttaatggtga tggatgatgt gtataacttc tgtttctgct ttctcttttt 60  
ca 62

&lt;210&gt; 482

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 482

atgggaacaa gagctctgca gtgtgaggtt tctcacactc atgaaaatga aaattatctc 60  
ttacatgaaa attgcatggt gaaaaaggaa attgccatgc taaaactgga aatagccaca 120  
ctgaaacacc aataccagga aaaggaaaat aaatactttg aggacattaa gattttaaaa 180  
gaaaagaatg ctgaacttca gatgacccta aaactgaaag aggaatcatt aactaaaagg 240  
gcatctcaat atagtgggca gcttaaagtt ctgatagctg agaacacaat gctcacttct 300  
aaattgaagg aaaaacaaga caaagaaata ctagaggcag aaattgaatc acaccatcct 360  
agactggcct ctgctgtaca agaccatgat caaattgtga catcaagaaa aagtcaagaa 420  
cctgctttcc acattgcagg agatgcttgt ttgcaaagaa aaatgaatgt tgatgtgagt 480  
agtacgatat ataacaatga ggtgctccat caaccacttt ctgaagctca aaggaaatcc 540  
aaaagcctaa aaattaatct caattatgcc ggagatgctc taagagaaaa tacattggtt 600  
tcagaacatg cacaagaga ccaacgtgaa acacagtgtc aaatgaagga agctgaacac 660  
atgtatcaaa acgaacaaga taatgtgaac aaacacactg aacagcagga gtctctagat 720  
cagaattat ttcaactaca aagcaaaaat atgtggcttc aacagcaatt agttcatgca 780  
cataagaaag ctgacaacaa aagcaagata acaattgata ttcattttct tgagaggaaa 840  
atgcaacatc atctcctaaa agagaaaaat gagagatat ttaattacaa taaccattta 900  
aaaaaccgta tatatcaata tgaaaaagag aaagcagaaa cagaagttat acatcatcac 960  
catcaccatt aa 972

&lt;210&gt; 483

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 483

Met	Gly	Thr	Arg	Ala	Leu	Gln	Cys	Glu	Val	Ser	His	Thr	His	Glu	Asn
1				5					10					15	
Glu	Asn	Tyr	Leu	Leu	His	Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala
		20						25					30		
Met	Leu	Lys	Leu	Glu	Ile	Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys
		35					40				45				
Glu	Asn	Lys	Tyr	Phe	Glu	Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala
		50				55					60				
Glu	Leu	Gln	Met	Thr	Leu	Lys	Leu	Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg
65					70				75					80	
Ala	Ser	Gln	Tyr	Ser	Gly	Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr
			85					90						95	
Met	Leu	Thr	Ser	Lys	Leu	Lys	Glu	Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu
		100						105					110		
Ala	Glu	Ile	Glu	Ser	His	His	Pro	Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp
		115					120					125			
His	Asp	Gln	Ile	Val	Thr	Ser	Arg	Lys	Ser	Gln	Glu	Pro	Ala	Phe	His
		130				135					140				
Ile	Ala	Gly	Asp	Ala	Cys	Leu	Gln	Arg	Lys	Met	Asn	Val	Asp	Val	Ser
145					150					155				160	
Ser	Thr	Ile	Tyr	Asn	Asn	Glu	Val	Leu	His	Gln	Pro	Leu	Ser	Glu	Ala
				165				170						175	

Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp  
 180 185 190  
 Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln  
 195 200 205  
 Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn  
 210 215 220  
 Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp  
 225 230 235 240  
 Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln  
 245 250 255  
 Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile  
 260 265 270  
 Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu  
 275 280 285  
 Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile  
 290 295 300  
 Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Val Ile His His His  
 305 310 315 320  
 His His His

&lt;210&gt; 484

&lt;211&gt; 1518

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 484

atgacctgcg gatcaggatt tgggtgggccc gccttccgct gcatctcggc ctgcggggccg 60  
 cggcccggcc gctgctgcat caccgccgcc ccctaccgtg gcatctcctg ctaccgccgc 120  
 ctcaccgggg gcttcggcag ccacagcgtg tgcggaggct ttcggggccg ctccctgcgga 180  
 cgcagcttcg gctaccgctc cggggggcgtg tgcggggcca gtcccccatt catcaccacc 240  
 gtgtcgggtca acgagagcct cctcacgccc ctcaacctgg agatcgaccc caacgcgcag 300  
 tgcgtgaagc aggaggagaa ggagcagatc aagtcctca acagcagggt cgcggccttc 360  
 atcgacaagg tgcgcttcct ggagcagcag aacaaactgc tggagacaaa gctgcagttc 420  
 taccagaacc gcgagtgttg ccagagcaac ctggagcccc tgtttgaggg ctacatcgag 480  
 actctgcggc gggaggccga gtgcgtggag gccgacagcg ggaggctggc ctcagagctt 540  
 aaccacgtgc aggaggtgct ggaggggtac aagaagaagt atgaggagga ggtttctctg 600  
 agagcaacag ctgagaacga gtttgtggct ctgaagaagg atgtggactg cgcctacctc 660  
 cgcaagtcag acctggaggc caacgtggag gccctgatcc aggagatcga ctccctgagg 720  
 cggctgtatg aggaggagat ccgcattctc cagtcgcaca tctcagacac ctccgtgggt 780  
 gtcaagctgg acaacagccg ggacctgaac atggactgca tcattgccga gattaaggca 840  
 cagtatgacg acattgtcac ccgcagccgg gccgaggccg agtcctggta ccgcagcaag 900  
 tgtgaggaga tgaaggccac ggtgatcagg cacggggaga ccctgcgccg caccaaggag 960  
 gagatcaatg agctgaaccg catgatccaa aggctgacgg ccgagggtgga gaatgccaag 1020  
 tgccagaact ccaagctgga ggccgcggtg gccagtcctg agcagcaggg tgaggcagcc 1080  
 ctcagtgatg cccgctgcaa gctggccgag ctggaggggc ccctgcagaa ggccaagcag 1140  
 gacatggcct gcctgatcag ggagtaccag gaggtgatga actccaagct gggcctggac 1200  
 atcgagatcg ccacctacag gcgcctgctg gagggcgagg agcagaggct atgtgaaggc 1260  
 attggggctg tgaatgtctg tgtcagcagc tcccggggcg gggtcgtgtg cggggacctc 1320  
 tgcgtgtcag gctcccggcc agtgactggc agtgtctgca gcgctccgtg caacgggaac 1380  
 gtggcggtga gcaccggcct gtgtgcgccc tgcggccaat tgaacaccac ctgcggaggg 1440  
 ggttcctcgc gcgtgggctc ctgtggtatc agctccctgg gtgtggggtc ttgcggcagc 1500  
 agctgccgga aatgttag 1518

&lt;210&gt; 485

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 485

```

Met Thr Cys Gly Ser Gly Phe Gly Gly Arg Ala Phe Arg Cys Ile Ser
 1           5           10           15
Ala Cys Gly Pro Arg Pro Gly Arg Cys Cys Ile Thr Ala Ala Pro Tyr
 20           25           30
Arg Gly Ile Ser Cys Tyr Arg Gly Leu Thr Gly Gly Phe Gly Ser His
 35           40           45
Ser Val Cys Gly Gly Phe Arg Ala Gly Ser Cys Gly Arg Ser Phe Gly
 50           55           60
Tyr Arg Ser Gly Gly Val Cys Gly Pro Ser Pro Pro Cys Ile Thr Thr
 65           70           75           80
Val Ser Val Asn Glu Ser Leu Leu Thr Pro Leu Asn Leu Glu Ile Asp
 85           90           95
Pro Asn Ala Gln Cys Val Lys Gln Glu Glu Lys Glu Gln Ile Lys Ser
100          105          110
Leu Asn Ser Arg Phe Ala Ala Phe Ile Asp Lys Val Arg Phe Leu Glu
115          120          125
Gln Gln Asn Lys Leu Leu Glu Thr Lys Leu Gln Phe Tyr Gln Asn Arg
130          135          140
Glu Cys Cys Gln Ser Asn Leu Glu Pro Leu Phe Glu Gly Tyr Ile Glu
145          150          155          160
Thr Leu Arg Arg Glu Ala Glu Cys Val Glu Ala Asp Ser Gly Arg Leu
165          170          175
Ala Ser Glu Leu Asn His Val Gln Glu Val Leu Glu Gly Tyr Lys Lys
180          185          190
Lys Tyr Glu Glu Val Ser Leu Arg Ala Thr Ala Glu Asn Glu Phe
195          200          205
Val Ala Leu Lys Lys Asp Val Asp Cys Ala Tyr Leu Arg Lys Ser Asp
210          215          220
Leu Glu Ala Asn Val Glu Ala Leu Ile Gln Glu Ile Asp Phe Leu Arg
225          230          235          240
Arg Leu Tyr Glu Glu Ile Arg Ile Leu Gln Ser His Ile Ser Asp
245          250          255
Thr Ser Val Val Val Lys Leu Asp Asn Ser Arg Asp Leu Asn Met Asp
260          265          270
Cys Ile Ile Ala Glu Ile Lys Ala Gln Tyr Asp Asp Ile Val Thr Arg
275          280          285
Ser Arg Ala Glu Ala Glu Ser Trp Tyr Arg Ser Lys Cys Glu Glu Met
290          295          300
Lys Ala Thr Val Ile Arg His Gly Glu Thr Leu Arg Arg Thr Lys Glu
305          310          315          320
Glu Ile Asn Glu Leu Asn Arg Met Ile Gln Arg Leu Thr Ala Glu Val
325          330          335
Glu Asn Ala Lys Cys Gln Asn Ser Lys Leu Glu Ala Ala Val Ala Gln
340          345          350
Ser Glu Gln Gln Gly Glu Ala Ala Leu Ser Asp Ala Arg Cys Lys Leu
355          360          365
Ala Glu Leu Glu Gly Ala Leu Gln Lys Ala Lys Gln Asp Met Ala Cys
370          375          380
Leu Ile Arg Glu Tyr Gln Glu Val Met Asn Ser Lys Leu Gly Leu Asp
385          390          395          400
Ile Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly Glu Glu Gln Arg
405          410          415
Leu Cys Glu Gly Ile Gly Ala Val Asn Val Cys Val Ser Ser Ser Arg
420          425          430
Gly Gly Val Val Cys Gly Asp Leu Cys Val Ser Gly Ser Arg Pro Val

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435 440 445  
 Thr Gly Ser Val Cys Ser Ala Pro Cys Asn Gly Asn Val Ala Val Ser  
 450 455 460  
 Thr Gly Leu Cys Ala Pro Cys Gly Gln Leu Asn Thr Thr Cys Gly Gly  
 465 470 475 480  
 Gly Ser Cys Gly Val Gly Ser Cys Gly Ile Ser Ser Leu Gly Val Gly  
 485 490 495  
 Ser Cys Gly Ser Ser Cys Arg Lys Cys  
 500 505

&lt;210&gt; 486

&lt;211&gt; 827

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 486

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 tgatcaggca cggggagacc ctgcccgcga ccaaggagga gatcaatgag ctgaaccgca 240  
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 agtaccagga ggtgatgaac tccaagctgg gcctggacat cgagatcgcc acctacaggc 480  
 gcctgctgga gggcgaggag cagaggctat gtgaaggcat tggggctgtg aatgtctgtg 540  
 tcagcagctc ccggggcggg gtcgtgtgcg gggacctctg cgtgtcaggc tcccggccag 600  
 tgactggcag tgtctgcagc gctccgtgca acgggaacgt ggcgggtgagc accggcctgt 660  
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 gtggtatcag ctccctgggt gtggggctct gcggcagcag ctgccggaaa tgtaggcac 780  
 cccaactcaa gtcccaggcc ccaggcatct ttcctgccct gccttgc 827

&lt;210&gt; 487

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 487

Met Asp Cys Ile Ile Ala Glu Ile Lys Ala Gln Tyr Asp Asp Ile Val  
 1 5 10 15  
 Thr Arg Ser Arg Ala Glu Ala Glu Ser Trp Tyr Arg Ser Lys Cys Glu  
 20 25 30  
 Glu Met Lys Ala Thr Val Ile Arg His Gly Glu Thr Leu Arg Arg Thr  
 35 40 45  
 Lys Glu Glu Ile Asn Glu Leu Asn Arg Met Ile Gln Arg Leu Thr Ala  
 50 55 60  
 Glu Val Glu Asn Ala Lys Cys Gln Asn Ser Lys Leu Glu Ala Ala Val  
 65 70 75 80  
 Ala Gln Ser Glu Gln Gln Gly Glu Ala Ala Leu Ser Asp Ala Arg Cys  
 85 90 95  
 Lys Leu Ala Glu Leu Glu Gly Ala Leu Gln Lys Ala Lys Gln Asp Met  
 100 105 110  
 Ala Cys Leu Ile Arg Glu Tyr Gln Glu Val Met Asn Ser Lys Leu Gly  
 115 120 125  
 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly Glu Glu  
 130 135 140  
 Gln Arg Leu Cys Glu Gly Ile Gly Ala Val Asn Val Cys Val Ser Ser  
 145 150 155 160

Ser Arg Gly Gly Val Val Cys Gly Asp Leu Cys Val Ser Gly Ser Arg  
 165 170 175  
 Pro Val Thr Gly Ser Val Cys Ser Ala Pro Cys Asn Gly Asn Val Ala  
 180 185 190  
 Val Ser Thr Gly Leu Cys Ala Pro Cys Gly Gln Leu Asn Thr Thr Cys  
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 Gly Gly Gly Ser Cys Gly Val Gly Ser Cys Gly Ile Ser Ser Leu Gly  
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 Val Gly Ser Cys Gly Ser Ser Cys Arg Lys Cys  
 225 230 235

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 <212> PRT  
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 1 5

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 <212> DNA  
 <213> Homo sapiens

<400> 489  
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<210> 490  
 <211> 3288  
 <212> DNA  
 <213> Homo sapiens

<400> 490  
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 ggctgcccct tattggagaa tgtgatttcc aagacaatca atccacaagt gtctaagact 120  
 gaatacaaaag aacttcttca agagttcata gacgacaatg ccactacaaa tgccatagat 180  
 gaattgaagg aatgttttct taaccaaacy gatgaaactc tgagcaatgt tgagggtgtt 240  
 atgcaattaa tatatgacag cagtctttgt gatttattta tgagtcccg c gcaaaagaaaca 300  
 tctgagaaat ttacgtgggc agcaaaagga agacctagga agatcgcatg ggagaaaaaa 360  
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 gaaaaaggaa gatctaagat gattgcatgt cctacaaaag aatcatctac aaaagcaagt 480  
 gccaatgatc agaggttccc atcagaatcc aaacaagagg aagatgaaga atattcttgt 540  
 gattctcgga gtctctttga gagttctgca aagattcaag tgtgtatacc tgagtctata 600  
 tatcaaaaag taatggagat aaatagagaa gtagaagagc ctcctaagaa gccatctgcc 660  
 ttcaagcctg ccattgaaat gcaaaactct gttccaaata aagccttga attgaagaat 720  
 gaacaaacat tgagagcaga tccgatgttc ccaccagaat ccaaacaaaa ggactatgaa 780  
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 aaagatgggc ttctgaaggc taactgcgga atgaaagttt ctattccaac taaagcctta 1320

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acattgagag cagatgagat actcccatca gaatccaac aaaaggacta tgaagaaagt 1500
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aaaatcttgg atacagtcca ttcttgtgaa agagcaaggg aacttcaaaa agatcactgt 2040
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&lt;210&gt; 491

&lt;211&gt; 2232

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 491

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gaatacaaaag aacttcttca agagttcata gacgacaatg ccactacaaa tgccatagat 180
gaattgaagg aatgttttct taaccaaacc gatgaaactc tgagcaatgt tgagggtgtt 240
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attgcatgtt ga 2232

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&lt;210&gt; 492

&lt;211&gt; 1233

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 492

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gaattgaagg aatgttttct taaccaaacg gatgaaactc tgagcaatgt tgagggtgtt 240
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aaaaaggaat ttgccatgct aaaactggaa atagccacac tgaacacca ataccaggaa 420
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agcaagataa caattgatat tcattttctt gagaggaaaa tgcaacatca tctcctaaaa 1140
gagaaaaatg aggagatatt taattacaat aaccatttaa aaaaccgtat atatcaatat 1200
gaaaaagaga aagcagaaac agaagttata taa 1233

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&lt;210&gt; 493

&lt;211&gt; 1095

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 403, 522, 615

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 493

Met	Lys	Leu	Leu	Met	Val	Leu	Met	Leu	Ala	Ala	Leu	Ser	Gln	His	Cys
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Tyr	Ala	Gly	Ser	Gly	Cys	Pro	Leu	Leu	Glu	Asn	Val	Ile	Ser	Lys	Thr
			20					25					30		
Ile	Asn	Pro	Gln	Val	Ser	Lys	Thr	Glu	Tyr	Lys	Glu	Leu	Leu	Gln	Glu
			35				40					45			
Phe	Ile	Asp	Asp	Asn	Ala	Thr	Thr	Asn	Ala	Ile	Asp	Glu	Leu	Lys	Glu
	50					55					60				
Cys	Phe	Leu	Asn	Gln	Thr	Asp	Glu	Thr	Leu	Ser	Asn	Val	Glu	Val	Phe
65					70					75					80
Met	Gln	Leu	Ile	Tyr	Asp	Ser	Ser	Leu	Cys	Asp	Leu	Phe	Met	Ser	Pro
				85					90					95	
Ala	Lys	Glu	Thr	Ser	Glu	Lys	Phe	Thr	Trp	Ala	Ala	Lys	Gly	Arg	Pro
			100					105					110		
Arg	Lys	Ile	Ala	Trp	Glu	Lys	Lys	Glu	Thr	Pro	Val	Lys	Thr	Gly	Cys
		115					120					125			
Val	Ala	Arg	Val	Thr	Ser	Asn	Lys	Thr	Lys	Val	Leu	Glu	Lys	Gly	Arg
	130					135					140				
Ser	Lys	Met	Ile	Ala	Cys	Pro	Thr	Lys	Glu	Ser	Ser	Thr	Lys	Ala	Ser
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Ala	Asn	Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Glu	Glu	Asp	Glu
			165						170					175	
Glu	Tyr	Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	Glu	Ser	Ser	Ala	Lys	Ile
			180					185					190		
Gln	Val	Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	Lys	Val	Met	Glu	Ile	Asn
		195					200					205			
Arg	Glu	Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	Ser	Ala	Phe	Lys	Pro	Ala
	210					215					220				
Ile	Glu	Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Ala	Phe	Glu	Leu	Lys	Asn
225					230					235					240
Glu	Gln	Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	Pro	Pro	Glu	Ser	Lys	Gln
			245						250					255	
Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr
		260						265					270		
Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu
		275					280					285			
Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn	Lys	Asp	Gly
	290					295					300				
Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala
305					310					315					320
Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Gly	Lys
			325						330					335	
Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn
		340						345					350		
Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile
		355					360					365			
Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp
	370					375					380				
Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro
385					390					395					400
Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu
			405						410					415	
Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys	Gly	Met	Lys
			420					425					430		
Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe
		435					440						445		

Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu  
 450 455 460  
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 485 490 495  
 Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser  
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 Gln Lys Asp Val Cys Leu Pro Lys Ala Xaa His Gln Lys Glu Ile Asp  
 515 520 525  
 Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu  
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 545 550 555 560  
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 565 570 575  
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 580 585 590  
 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro  
 595 600 605  
 Ser Glu Ser Lys Gln Lys Xaa Val Glu Glu Asn Ser Trp Asp Ser Glu  
 610 615 620  
 Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala  
 625 630 635 640  
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 645 650 655  
 Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala  
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 Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu  
 675 680 685  
 Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala  
 690 695 700  
 Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln  
 705 710 715 720  
 Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg  
 725 730 735  
 Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg  
 740 745 750  
 Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu  
 755 760 765  
 Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn  
 770 775 780  
 Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His  
 785 790 795 800  
 Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile  
 805 810 815  
 Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu  
 820 825 830  
 Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu  
 835 840 845  
 Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly  
 850 855 860  
 Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu  
 865 870 875 880  
 Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His  
 885 890 895  
 His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr  
 900 905 910

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Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys
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Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn
    930                      935                      940
Glu Val Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser
    945                      950                      955                      960
Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr
    965                      970                      975
Leu Val Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln
    980                      985                      990
Met Lys Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn
    995                      1000                      1005
Lys His Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu
    1010                      1015                      1020
Gln Ser Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys
    1025                      1030                      1035                      1040
Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu
    1045                      1050                      1055
Arg Lys Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe
    1060                      1065                      1070
Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu
    1075                      1080                      1085
Lys Ala Glu Thr Glu Asn Ser
    1090                      1095

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&lt;210&gt; 494

&lt;211&gt; 743

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 403, 522, 615

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 494

```

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys
 1                      5                      10                      15
Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
    20                      25                      30
Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
    35                      40                      45
Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
    50                      55                      60
Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
    65                      70                      75                      80
Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe Met Ser Pro
    85                      90                      95
Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro
    100                      105                      110
Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys
    115                      120                      125
Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg
    130                      135                      140
Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser
    145                      150                      155                      160
Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu

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625          630          635          640
Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser
          645          650          655
Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala
          660          665          670
Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu
          675          680          685
Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala
          690          695          700
Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln
705          710          715          720
Glu Leu Cys Ser Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile
          725          730          735
Ser Tyr Met Lys Ile Ala Cys
          740

```

```

<210> 495
<211> 410
<212> PRT
<213> Homo sapiens

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```

<400> 495
Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys
 1          5          10          15
Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
          20          25          30
Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
          35          40          45
Phe Ile Asp Asp Asn Ala Thr Asn Ala Ile Asp Glu Leu Lys Glu
          50          55          60
Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
65          70          75          80
Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe Met Gly Thr
          85          90          95
Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn Glu Asn Tyr
          100          105          110
Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys
          115          120          125
Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys
130          135          140
Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln
145          150          155          160
Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln
          165          170          175
Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr
          180          185          190
Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile
          195          200          205
Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln
210          215          220
Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly
225          230          235          240
Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile
          245          250          255
Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys
          260          265          270
Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg

```

275	280	285
Glu Asn Thr Leu Val Ser	Glu His Ala Gln Arg Asp	Gln Arg Glu Thr
290	295	300
Gln Cys Gln Met Lys Glu	Ala Glu His Met Tyr	Gln Asn Glu Gln Asp
305	310	315
Asn Val Asn Lys His Thr	Glu Gln Gln Glu Ser	Leu Asp Gln Lys Leu
325	330	335
Phe Gln Leu Gln Ser Lys	Asn Met Trp Leu Gln	Gln Gln Leu Val His
340	345	350
Ala His Lys Lys Ala Asp	Asn Lys Ser Lys Ile Thr	Ile Asp Ile His
355	360	365
Phe Leu Glu Arg Lys Met	Gln His His Leu Leu Lys	Glu Lys Asn Glu
370	375	380
Glu Ile Phe Asn Tyr Asn	Asn His Leu Lys Asn	Arg Ile Tyr Gln Tyr
385	390	395
Glu Lys Glu Lys Ala Glu	Thr Glu Val Ile	
405	410	

<210> 496  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 496  
 Ile Asp Glu Leu Lys Glu Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu  
 1 5 10 15  
 Ser Asn Val Glu  
 20

<210> 497  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 497  
 Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys Phe Leu Asn Gln  
 1 5 10 15

<210> 498  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 498  
 Ser Gln His Cys Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val  
 1 5 10 15  
 Ile Ser Lys Thr Ile  
 20

<210> 499  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 499

Glu Tyr Lys Glu Leu Leu Gln Glu Phe Ile Asp Asp Asn Ala Thr Thr  
 1 5 10 15  
 Asn Ala Ile Asp  
 20

&lt;210&gt; 500

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 500

Lys Leu Leu Met Val Leu Met Leu Ala  
 1 5

&lt;210&gt; 501

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 501

Gln Glu Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile  
 1 5 10

&lt;210&gt; 502

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 502

Leu Lys Glu Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu  
 1 5 10

&lt;210&gt; 503

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 503

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys  
 1 5 10 15  
 Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr  
 20 25 30  
 Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu  
 35 40 45  
 Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu  
 50 55 60  
 Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe  
 65 70 75 80  
 Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe  
 85 90

&lt;210&gt; 504

&lt;211&gt; 1964

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 504

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gcacgtctga cgccccatgt gctgaaagg cgaggagcct cctgcggcgg cccctgtgtc 60
cctgcctcta cctgcgcacc tgcacgtgtt caacccccgg gagaacacct ggccggccct 120
gaccagagtg cccgaggagg ccccgcttcg gggctgcggg ctctgcacca tgcacaacta 180
cctgtttctg gcggggggca tccgtggctc cggtgccaag gccgtctgct ccaacgaggt 240
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gtacagcatg gagtgctacg acccgcgaa agacgcctgg accccacggc gcgcaactccc 420
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cgggggtcac ctcttctacc gcctgctcag gtacagcccc gtgaaggatg cttgggacga 540
gtgcccatac agtgccagcc accggcgctt cagcgacatc gttgcactgg ggggcttcc 600
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gaggaggggg tagaaaacat tcacacttcc tatgtctgtt cagcaggaca gggagcaaaa 1320
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actgtgctcc actccaacct ccagcctgga tgtccctgtc tgggcccttt ttctgttttt 1920
tattctatgt tcagcaccac tggcaccaaa tacattttaa ttca 1964
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&lt;210&gt; 505

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 505

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atgcacaact acctgtttct ggccgggggg atccgtggct ccggtgccaa ggccgtctgc 60
tccaacgagg tcttctgcta caaccctctg accaactctt ggagccaggt tcggcccatg 120
cagcaggccc gagccagct caagctggtg gccctggacg ggctgctcta tgccatcggt 180
ggcgaatgcc tgtacagcat ggagtgtac gacccgcgaa cagacgcctg gacccacgc 240
gcgcccactc ccgaggcac ctctccctgt gcccacgagg ctgtggcctg ccgtggggac 300
atctacgtca ccgggggtca cctcttctac cgcctgctca ggtacagccc cgtgaaggat 360
gcttgggacg agtgcccata cagtgcacg caccggcggt ccagcgacat cgttgcaactg 420
gggggcttcc tgtaccgctt cgacctgtcg cggggcggtg gcgcccggct gatgcgtac 480
aacacagtga ccggctcctg gagcagggtt gcctccctgc cctgcccgc ccccgcccca 540
ctgcgctgca ccacctggg caacaccatt tactgcctca accccagggt cactgccacc 600
ttcacggctc ctggggggac tgcccagttc caggccaagg agctgcagcc cttcccttg 660
gggagcaccg gggctcctcag tccattcatc ctgactctgc cccctgagga ccggctgcag 720
acctcactct ga 732
```

<210> 506  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<400> 506  
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 tccaacgagg tcttctgcta caaccctctg accaaccatct ggagccaggt tcggcccatg 120  
 cagcaggccc gagcccagct caagctgggt gccctggacg ggctgctcta tgccatcggt 180  
 ggcgaaatgcc tgtacagcat ggagtgtac gaccgcgaa cagacgcctg gacccacgc 240  
 gcgccactcc ccgcaggcac ctccctgtg gccacgagg ctgtggcctg ccgtggggac 300  
 atctacgtca ccgggggtca cctcttctac cgcctgtca ggtacagccc cgtgaaggat 360  
 gcttgggacg agtgccata cagtgccagc caccggcgtt ccagcgacat cgttgactg 420  
 gggggcttcc tgtaccgctt cgacctgtg cggggcgtg gcgccgcgt gatgcgtac 480  
 aacacagtga ccggctcctg gagcagggt gcctccctgc ccctgccgc ccccgccca 540  
 ctgcgtgca ccacctggg caacaccatt tactgcctca accccaggt cactgccacc 600  
 ttcacggtct ctggggggac tgcccagttc caggccaagg agctgcagcc cttcccctt 660  
 gggagcaccg gggtcctcag tccattcatc ctgactctgc cccctgagga ccggctgcag 720  
 acctcactc 729

<210> 507  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 507  
 Met His Asn Tyr Leu Phe Leu Ala Gly Gly Ile Arg Gly Ser Gly Ala  
 1 5 10 15  
 Lys Ala Val Cys Ser Asn Glu Val Phe Cys Tyr Asn Pro Leu Thr Asn  
 20 25 30  
 Ile Trp Ser Gln Val Arg Pro Met Gln Gln Ala Arg Ala Gln Leu Lys  
 35 40 45  
 Leu Val Ala Leu Asp Gly Leu Leu Tyr Ala Ile Gly Gly Glu Cys Leu  
 50 55 60  
 Tyr Ser Met Glu Cys Tyr Asp Pro Arg Thr Asp Ala Trp Thr Pro Arg  
 65 70 75 80  
 Ala Pro Leu Pro Ala Gly Thr Phe Pro Val Ala His Glu Ala Val Ala  
 85 90 95  
 Cys Arg Gly Asp Ile Tyr Val Thr Gly Gly His Leu Phe Tyr Arg Leu  
 100 105 110  
 Leu Arg Tyr Ser Pro Val Lys Asp Ala Trp Asp Glu Cys Pro Tyr Ser  
 115 120 125  
 Ala Ser His Arg Arg Ser Ser Asp Ile Val Ala Leu Gly Gly Phe Leu  
 130 135 140  
 Tyr Arg Phe Asp Leu Leu Arg Gly Val Gly Ala Ala Val Met Arg Tyr  
 145 150 155 160  
 Asn Thr Val Thr Gly Ser Trp Ser Arg Ala Ser Leu Pro Leu Pro  
 165 170 175  
 Ala Pro Ala Pro Leu Arg Cys Thr Thr Leu Gly Asn Thr Ile Tyr Cys  
 180 185 190  
 Leu Asn Pro Gln Val Thr Ala Thr Phe Thr Val Ser Gly Gly Thr Ala  
 195 200 205  
 Gln Phe Gln Ala Lys Glu Leu Gln Pro Phe Pro Leu Gly Ser Thr Gly  
 210 215 220  
 Val Leu Ser Pro Phe Ile Leu Thr Leu Pro Pro Glu Asp Arg Leu Gln  
 225 230 235 240  
 Thr Ser Leu

<210> 508  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 508  
 Met His Asn Tyr Leu Phe Leu Ala Gly Gly Ile Arg Gly Ser Gly Ala  
 1 5 10 15  
 Lys Ala Val Cys Ser Asn Glu Val Phe Cys Tyr Asn Pro Leu Thr Asn  
 20 25 30  
 Ile Trp Ser Gln Val Arg Pro Met Gln Gln Ala Arg Ala Gln Leu Lys  
 35 40 45  
 Leu Val Ala Leu Asp Gly Leu Leu Tyr Ala Ile Gly Gly Glu Cys Leu  
 50 55 60  
 Tyr Ser Met Glu Cys Tyr Asp Pro Arg Thr Asp Ala Trp Thr Pro Arg  
 65 70 75 80  
 Ala Pro Leu Pro Ala Gly Thr Phe Pro Val Ala His Glu Ala Val Ala  
 85 90 95  
 Cys Arg Gly Asp Ile Tyr Val Thr Gly Gly His Leu Phe Tyr Arg Leu  
 100 105 110  
 Leu Arg Tyr Ser Pro Val Lys Asp Ala Trp Asp Glu Cys Pro Tyr Ser  
 115 120 125  
 Ala Ser His Arg Arg Ser Ser Asp Ile Val Ala Leu Gly Gly Phe Leu  
 130 135 140  
 Tyr Arg Phe Asp Leu Leu Arg Gly Val Gly Ala Ala Val Met  
 145 150 155

<210> 509  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 509  
 Arg Tyr Asn Thr Val Thr Gly Ser Trp Ser Arg Ala Ala Ser Leu Pro  
 1 5 10 15  
 Leu Pro Ala Pro Ala Pro Leu Arg Cys Thr Thr Leu Gly Asn Thr Ile  
 20 25 30  
 Tyr Cys Leu Asn Pro Gln Val Thr Ala Thr Phe Thr Val Ser Gly Gly  
 35 40 45  
 Thr Ala Gln Phe Gln Ala Lys Glu Leu Gln Pro Phe Pro Leu Gly Ser  
 50 55 60  
 Thr Gly Val Leu Ser Pro Phe Ile Leu Thr Leu Pro Pro Glu Asp Arg  
 65 70 75 80  
 Leu Gln Thr Ser Leu  
 85

<210> 510  
 <211> 732  
 <212> DNA  
 <213> Homo sapiens

<400> 510  
 atgcgacccc agggcccccgc cgcctccccg cagcggctcc gcggcctcct gctgctcctg 60

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ctgctgcagc tgcccgcgcc gtcgagcgcc tctgagatcc ccaaggggaa gcaaaaggcg 120
cagctccggc agagggaggt ggtggacctg tataatggaa tgtgcttaca agggccagca 180
ggagtgcctg gtcgagacgg gagccctggg gccaatgtta ttccgggtac acctgggato 240
ccaggctcgg atggattcaa aggagaaaag ggggaatgtc tgagggaaaag ctttgaggag 300
tcctggacac ccaactacaa gcagtgttca tggagtcat tgaattatgg catagatctt 360
gggaaaattg cggagtgtac atttacaaag atgcgttcaa atagtctctt aagagttttg 420
ttcagtggct cacttcggct aaaatgcaga aatgcattgt gtcagcgttg gtatttcaca 480
ttcaatggag ctgaatgttc aggacctctt cccattgaag ctataattta tttggacca 540
ggaagccctg aaatgaattc aacaattaat attcatcgca cttctctgtt ggaaggactt 600
tgtgaaggaa ttggtgctgg attagtggat gttgctatct gggttggcac ttgttcagat 660
taccctaaaag gagatgcttc tactggatgg aattcagttt ctcgcatcat tattgaagaa 720
ctacccaaat aa 732

```

&lt;210&gt; 511

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 511

```

atgcgacccc agggcccccgc cgcctccccg cagcggctcc ggggcctcct gctgctcctg 60
ctgctgcagc tgcccgcgcc gtcgagcgcc tctgagatcc ccaaggggaa gcaaaaggcg 120
cagctccggc agagggaggt ggtggacctg tataatggaa tgtgcttaca agggccagca 180
ggagtgcctg gtcgagacgg gagccctggg gccaatgtta ttccgggtac acctgggato 240
ccaggctcgg atggattcaa aggagaaaag ggggaatgtc tgagggaaaag ctttgaggag 300
tcctggacac ccaactacaa gcagtgttca tggagtcat tgaattatgg catagatctt 360
gggaaaattg cggagtgtac atttacaaag atgcgttcaa atagtctctt aagagttttg 420
ttcagtggct cacttcggct aaaatgcaga aatgcattgt gtcagcgttg gtatttcaca 480
ttcaatggag ctgaatgttc aggacctctt cccattgaag ctataattta tttggacca 540
ggaagccctg aaatgaattc aacaattaat attcatcgca cttctctgtt ggaaggactt 600
tgtgaaggaa ttggtgctgg attagtggat gttgctatct gggttggcac ttgttcagat 660
taccctaaaag gagatgcttc tactggatgg aattcagttt ctcgcatcat tattgaagaa 720
ctacccaaa 729

```

&lt;210&gt; 512

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 512

```

atgcagcctg cggcggcctc ggagcgcggc ggagcagacg ctgaccacgt tcctctcctc 60
ggtctcctcc gcctccagct ccgcgctgcc cggcagccgg gagccatgcy accccaggcg 120
cccgcgcct cccgcgcagc gctccgcggc ctctctgctg tcctgctgct gcagctgccc 180
gcgcctcga gcgcctctga gatccccaa gggaaagcaa aggcgcagct ccggcagagg 240
gagtggttg acctgtataa tggaaatgtc ttacaagggc cagcaggagt gcctggtcga 300
gacgggagcc ctggggccaa tgttattccg ggtacacctg ggatcccagg tcgggatgga 360
ttcaaaggag aaaaggggga atgtctgagg gaaagctttg aggagtctg gacacccaac 420
tacaagcagt gttcatggag ttcaatgaat tatggcatag atcttgggaa aattgcggag 480
tgtacattta caaagatgcy ttcaaatagt gctctaagag ttttgttcag tggctcactt 540
cggctaaaat gcagaaatgc atgctgtcag cgttggtatt tcacattcaa tggagctgaa 600
tgttcaggac ctcttcccat tgaagctata atttatttgg accaagggaag ccctgaaatg 660
aattcaacaa ttaatatcca tcgcacttct tctgtggaag gactttgtga aggaattggt 720
gctggattag tggatgttgc tatctgggtt ggcacttggt cagattaccc aaaaggagat 780
gctctactg gatggaattc agtttctcgc atcattattg aagaactacc aaaataa 837

```

&lt;210&gt; 513

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 513

```

atgcagcctg cggcggcctc ggagcgcggc ggagcagacg ctgaccacgt tcctctcctc 60
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cccgcgcgct cccgcgagcg gctccgcggc ctctctgtgc tctgtctgtc gcagctgccc 180
gcgcgctcga gcgcctctga gatccccaag gggaagcaaa aggcgcagct ccggcagagg 240
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gacgggagcc ctggggccaa tgttattccg ggtacacctg ggatcccagg tcgggatgga 360
ttcaaaggag aaaaggggga atgtctgagc gaaaagctttg aggagtctcg gacaccaaac 420
tacaagcagt gttcatggag ttcatatgaat tatggcatag atcttgggaa aattgcggag 480
tgtacattta caaagatgag ttcaaatagt gctctaagag ttttgttcag tggctcactt 540
cggctaaaaat gcagaaatgc atgctgtcag cgttggtatt tcacattcaa tggagctgaa 600
tggtcaggac ctcttcccat tgaagctata atttatttgg accaaggaag ccctgaaatg 660
aattcaacaa ttaatatcca tcgcacttct tctgtggaag gactttgtga aggaattggt 720
gctggattag tggatgttgc tatctgggtt ggcacttggt cagattaccc aaaaggagat 780
gcttctactg gatggaattc agtttctcgc atcattattg aagaactacc aaaataa 837

```

&lt;210&gt; 514

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 514

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Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
 1           5           10           15
Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
 20           25           30
Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
 35           40           45
Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
 50           55           60
Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr Pro Gly Ile
 65           70           75           80
Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
 85           90           95
Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
100          105          110
Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
115          120          125
Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
130          135          140
Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
145          150          155          160
Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
165          170          175
Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
180          185          190
Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
195          200          205
Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
210          215          220
Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
225          230          235          240
Leu Pro Lys

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&lt;210&gt; 515

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 515

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Met Gln Pro Ala Ala Ala Ser Glu Arg Gly Gly Ala Asp Ala Asp His
              5              10              15
Val Pro Leu Leu Gly Leu Leu Arg Leu Gln Leu Arg Ala Ala Arg Gln
              20              25              30
Pro Gly Ala Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu
              35              40              45
Arg Gly Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser
              50              55              60
Ala Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
              65              70              75              80
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly
              85              90              95
Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr
              100              105              110
Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys
              115              120              125
Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys
              130              135              140
Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu
              145              150              155              160
Cys Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe
              165              170              175
Ser Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp
              180              185              190
Tyr Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu
              195              200              205
Ala Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile
              210              215              220
Asn Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly
              225              230              235              240
Ala Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr
              245              250              255
Pro Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile
              260              265              270
Ile Glu Glu Leu Pro Lys
              275

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&lt;210&gt; 516

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 516

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Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
              5              10              15
Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
              20              25              30
Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
              35              40              45
Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
              50              55              60
Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr Pro Gly Ile
              65              70              75              80

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<210> 517
<211> 232
<212> PRT
<213> Homo sapiens
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<400>	517															
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Pro	Gly	Ala	Met 35	Arg	Pro	Gln	Gly 40	Pro	Ala	Ala	Ser	Pro	Gln 45	Arg	Leu	
Arg	Gly 50	Leu	Leu	Leu	Leu	Leu 55	Leu	Gln	Leu	Pro 60	Ala	Pro	Ser	Ser		
Ala	Ser	Glu	Ile	Pro 70	Lys	Gly	Lys	Gln	Lys 75	Ala	Gln	Leu	Arg	Gln	Arg	
Glu	Val	Val	Asp 85	Tyr	Asn	Gly	Met	Cys 90	Leu	Gln	Gly	Pro	Ala 95	Gly		
Val	Pro	Gly	Arg 100	Asp	Gly	Ser	Pro	Gly 105	Ala	Asn	Val	Ile	Pro 110	Gly	Thr	
Pro	Gly	Ile	Pro 115	Gly	Arg	Asp	Gly	Phe 120	Lys	Gly	Glu	Lys 125	Gly	Glu	Cys	
Leu	Arg	Glu	Ser 130	Phe	Glu	Glu 135	Ser	Trp	Thr	Pro 140	Asn	Tyr	Lys	Gln	Cys	
Ser	Trp	Ser	Ser 145	Leu	Asn 150	Tyr	Gly	Ile	Asp 155	Leu	Gly	Lys	Ile	Ala	Glu	
Cys	Thr	Phe	Thr 165	Lys	Met	Arg	Ser	Asn 170	Ser	Ala	Leu	Arg	Val 175	Leu	Phe	
Ser	Gly	Ser	Leu 180	Arg	Leu	Lys	Cys	Arg 185	Asn	Ala	Cys	Cys	Gln 190	Arg	Trp	
Tyr	Phe	Thr 195	Phe	Asn	Gly	Ala	Glu 200	Cys	Ser	Gly	Pro	Leu 205	Pro	Ile	Glu	
Ala	Ile	Ile	Tyr 210	Leu	Asp 215	Gln	Gly	Ser	Pro	Glu	Met 220	Asn	Ser	Thr	Ile	
Asn	Ile	His	Arg	Thr 225	Ser 230	Ser	Val									

<210>	518
<211>	46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 518

Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	Val	Ala	Ile
			5						10					15	
Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	Ala	Ser	Thr	Gly
		20						25					30		
Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	Leu	Pro	Lys		
		35					40					45			

&lt;210&gt; 519

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 519

Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val
				5					10					15	
Ser	Arg	Ile	Ile	Ile	Glu	Glu	Leu	Pro	Lys						
		20						25							

&lt;210&gt; 520

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 520

aaaaatgagg agatatttaa ttacaataac catttaaaaa accgtatata tcaatatgaa 60

&lt;210&gt; 521

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 521

atgcaacatc atctcctaaa agagaaaaat gaggagatat ttaattacaa taaccattta 60

&lt;210&gt; 522

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 522

gacaacaaaa gcaagataac aattgatatt cattttcttg agaggaaaat gcaacatcat 60

&lt;210&gt; 523

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 523

aaaaatatgt ggcttcaaca gcaattagtt catgcacata agaaagctga caacaaaagc 60

&lt;210&gt; 524

&lt;211&gt; 63

<212> DNA

<213> Homo sapiens

<400> 524

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gca 63

<210> 525

<211> 60

<212> DNA

<213> Homo sapiens

<400> 525

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<210> 526

<211> 63

<212> DNA

<213> Homo sapiens

<400> 526

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<210> 527

<211> 60

<212> DNA

<213> Homo sapiens

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<211> 60

<212> DNA

<213> Homo sapiens

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<210> 529

<211> 60

<212> DNA

<213> Homo sapiens

<400> 529

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<211> 60

<212> DNA

<213> Homo sapiens

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<211> 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

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&lt;210&gt; 532

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

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&lt;210&gt; 533

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 533

aattgcatgt tgaaaaagga aattgccatg ctaaaactgg aaatagccac actgaaacac 60  
caa 63

&lt;210&gt; 534

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 534

Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala  
5 10 15  
Thr Leu Lys His Gln  
20

&lt;210&gt; 535

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 535

Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile  
5 10 15  
Lys Ile Leu Lys  
20

&lt;210&gt; 536

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 536

Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala  
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Glu Leu Gln Met  
20

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<213> Homo sapiens

<400> 537  
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Arg Lys Met Asn  
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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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Gln Arg Lys Ser  
                  20

<210> 541  
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<212> PRT  
<213> Homo sapiens

<400> 541  
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Asp Ala Leu Arg Glu

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&lt;210&gt; 542

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 542

Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser  
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20

&lt;210&gt; 543

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 543

Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln  
5 10 15Gln Leu Val His Ala  
20

&lt;210&gt; 544

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 544

Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala  
5 10 15Asp Asn Lys Ser  
20

&lt;210&gt; 545

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 545

Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys  
5 10 15Met Gln His His  
20

&lt;210&gt; 546

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 546

Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr

173

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 <212> PRT  
 <213> Homo sapiens  
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&lt;210&gt; 549

&lt;211&gt; 1953

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 985

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 549

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<211> 978

<212> DNA

<213> Homo sapiens

<400> 550

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caacagcatt	tagttcatgc	acataagaaa	gctgacaaca	aaagcaagat	aacaattgat	840
attcattttc	ttagaggaaa	aatgcaacat	catctcctaa	aagagaaaaa	tgaggagata	900
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acagaagtta	tataatag					978

**<210> 551**

**<211> 324**

<212> PRT

<213> Homo sapiens

**<400> 551**

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Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys  
20 25 30

Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu  
35 40 45

Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys  
50 55 60

Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys  
65 70 75 80

Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys  
85 90 95

Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr	Ser	Lys	Leu	Lys	Glu	Lys
			100					105					110		

Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg  
115 120 125

Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys  
 130 135 140  
 Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg  
 145 150 155 160  
 Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu  
 165 170 175  
 His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile  
 180 185 190  
 Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser  
 195 200 205  
 Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu  
 210 215 220  
 Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr  
 225 230 235 240  
 Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys  
 245 250 255  
 Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp  
 260 265 270  
 Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met  
 275 280 285  
 Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn  
 290 295 300  
 Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu  
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 Thr Glu Val Ile

&lt;210&gt; 552

&lt;211&gt; 661

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 552

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 20 25 30  
 Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala  
 35 40 45  
 Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys  
 50 55 60

Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn  
 65 70 75 80  
 Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr  
 85 90 95  
 Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val  
 100 105 110  
 Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu  
 115 120 125  
 Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu  
 130 135 140  
 Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln  
 145 150 155 160  
 Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp  
 165 170 175  
 Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser  
 180 185 190  
 Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp  
 195 200 205  
 Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu  
 210 215 220  
 Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu  
 225 230 235 240  
 Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gly Lys Pro Ser  
 245 250 255  
 Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala  
 260 265 270  
 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro  
 275 280 285  
 Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Thr Glu  
 290 295 300  
 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala  
 305 310 315 320  
 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser  
 325 330 335  
 Pro Gly Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser  
 340 345 350  
 Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala  
 355 360 365

Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln  
 370 375 380  
 Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu  
 385 390 395 400  
 Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu  
 405 410 415  
 Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys  
 420 425 430  
 Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile  
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 Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ser  
 450 455 460  
 Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met  
 465 470 475 480  
 Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe  
 485 490 495  
 Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu  
 500 505 510  
 Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu  
 515 520 525  
 Ser Lys Gln Lys Asn Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu  
 530 535 540  
 Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His  
 545 550 555 560  
 Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser  
 565 570 575  
 Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu  
 580 585 590  
 Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met  
 595 600 605  
 Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu  
 610 615 620  
 Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu  
 625 630 635 640  
 Cys Ser Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr  
 645 650 655  
 Met Lys Ile Ala Cys  
 660

Met Gln His His His His His Val Gly Ser Met Ser Pro Ala Lys  
5 10 15

Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala  
35 40 45

Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys  
50 55 60

Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn  
65 70 75 80

Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr  
85 90 95

Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val  
100 105 110

Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu  
115 120 125

Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu  
130 135 140

Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln  
145 150 155 160

Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp  
165 170 175

Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser  
180 185 190

Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp  
195 200 205

Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu  
210 215 220

Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu  
225 230 235 240

Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gly Lys Pro Ser  
245 250 255

Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala  
260 265 270

Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro

275					280					285					
Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Thr	Glu
290					295					300					
Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala
305					310					315					320
Ala	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Gly	Ser
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Pro	Gly	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys	Gly	Met	Lys	Val	Ser
			340					345					350		
Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala
			355					360					365		
Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln
			370				375					380			
Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu
385				390					395						400
Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu
				405					410					415	
Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys
			420					425					430		
Asp	Val	Cys	Leu	Pro	Lys	Ala	Ala	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile
			435				440					445			
Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	Gly	Phe	Leu	Lys	Ser
			450				455					460			
Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met
465				470					475						480
Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe
				485					490					495	
Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu
			500					505					510		
Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	Phe	Pro	Ser	Glu
			515				520					525			
Ser	Lys	Gln	Lys	Asn	Val	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu
			530				535					540			
Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	Lys	Ala	Thr	His
545				550					555						560
Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu	Asp	Ser	Thr	Ser
				565					570					575	
Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu	Arg	Ala	Arg	Glu
			580					585					590		

Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met  
 595 600 605  
 Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu  
 610 615 620  
 Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu  
 625 630 635 640  
 Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Lys Arg Arg Asn  
 645 650 655  
 Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu  
 660 665 670  
 Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala  
 675 680 685  
 Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn  
 690 695 700  
 Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn  
 705 710 715 720  
 Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr  
 725 730 735  
 Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile  
 740 745 750  
 Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu  
 755 760 765  
 Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu  
 770 775 780  
 Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu  
 785 790 795 800  
 Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro  
 805 810 815  
 Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg  
 820 825 830  
 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln  
 835 840 845  
 Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val  
 850 855 860  
 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys  
 865 870 875 880  
 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val  
 885 890 895

Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys  
                   900                                  905                                  910  
 Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His  
                   915                                  920                                  925  
 Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser  
                   930                                  935                                  940  
 Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala  
                   945                                  950                                  955                                  960  
 Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys  
                                   965                                  970                                  975  
 Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr  
                   980                                  985                                  990  
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 Glu Thr Glu Val Ile  
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<210> 554  
 <211> 25  
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<220>  
 <223> PCR primer

<400> 554  
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25

<210> 555  
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<400> 555  
 cgagaattca atacttaaga agaccatctt taccag

36

<210> 556  
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<400> 556  
cataagctta aggctaactg cggaatgaaa g 31

<210> 557  
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ccgcagaat tcaacatgca attttcatgt aagag 35

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<400> 558  
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<220>  
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<400> 560  
ggggaattgt gagcggataa caattc 26

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<400> 561  
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<400> 563  
gaggcccaa ggggttatgc tag 23

<210> 564  
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<212> DNA  
<213> Homo sapiens

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atcaacctta atatacaaga cggccagaag aggactgctc tacactgggc ctgtgtcaat 180  
ggccatgagg aagtagtaac atttctggta gacagaaagt gccagcttga cgtccttgat 240  
ggcgaacaca ggacacctct gatgaaggct ctacaatgcc atcaggaggc ttgtgcaaat 300  
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agcagacatc attcaatcca accagaatct cgctctgcac tccagcctag gtgacagagt 4440
gagactccac ctcgga 4458

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&lt;210&gt; 565

&lt;211&gt; 1341

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 565

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Met Thr Lys Arg Lys Lys Thr Ile Asn Leu Asn Ile Gln Asp Ala Gln
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Lys Arg Thr Ala Leu His Trp Ala Cys Val Asn Gly His Glu Glu Val
      20                      25                      30

Val Thr Phe Leu Val Asp Arg Lys Cys Gln Leu Asp Val Leu Asp Gly
      35                      40                      45

Glu His Arg Thr Pro Leu Met Lys Ala Leu Gln Cys His Gln Glu Ala
      50                      55                      60

Cys Ala Asn Ile Leu Ile Asp Ser Gly Ala Asp Ile Asn Leu Val Asp
      65                      70                      75                      80

Val Tyr Gly Asn Met Ala Leu His Tyr Ala Val Tyr Ser Glu Ile Leu
      85                      90                      95

Ser Val Val Ala Lys Leu Leu Ser His Gly Ala Val Ile Glu Val His
      100                     105                     110

Asn Lys Ala Ser Leu Thr Pro Leu Leu Leu Ser Ile Thr Lys Arg Ser
      115                     120                     125

Glu Gln Ile Val Glu Phe Leu Leu Ile Lys Asn Ala Asn Ala Asn Ala
      130                     135                     140

Val Asn Lys Tyr Lys Cys Thr Ala Leu Met Leu Ala Val Cys His Gly
      145                     150                     155                     160

Ser Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe
      165                     170                     175

Ala Ala Asp Ile Cys Gly Val Thr Ala Glu His Tyr Ala Val Thr Cys
      180                     185                     190

Gly Phe His His Ile His Glu Gln Ile Met Glu Tyr Ile Arg Lys Leu
      195                     200                     205

Ser Lys Asn His Gln Asn Thr Asn Pro Glu Gly Thr Ser Ala Gly Thr
      210                     215                     220

Pro Asp Glu Ala Ala Pro Leu Ala Glu Arg Thr Pro Asp Thr Ala Glu
      225                     230                     235                     240

Ser Leu Val Glu Lys Thr Pro Asp Glu Ala Ala Pro Leu Val Glu Arg
      245                     250                     255

Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu Ala
      260                     265                     270

Ala Ser Leu Val Glu Gly Thr Ser Asp Lys Ile Gln Cys Leu Glu Lys
      275                     280                     285

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Ala Thr Ser Gly Lys Phe Glu Gln Ser Ala Glu Glu Thr Pro Arg Glu  
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 Ile Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala  
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 Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Asp Thr Pro  
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 Glu Ser Ser Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln  
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 Lys Val Met Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro  
 450 455 460  
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 Pro Pro Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser  
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 Ser Ile Pro Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys  
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 Ala Glu Pro Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met  
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 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr

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Glu Glu Asn Ser Trp Asp Thr	Glu Ser Leu Cys Glu Thr Val Ser Gln	
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Lys Asp Val Cys Leu Pro Lys Ala Ala His	Gln Lys Glu Ile Asp Lys	
645	650	655
Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys		
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Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu		
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Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala		
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Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu		
705	710	715 720
Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser		
725	730	735
Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser		
740	745	750
Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr		
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His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro		
770	775	780
Asp Asn Asp Gly Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile		
785	790	795 800
Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu		
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Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys		
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Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg		
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Ala Asp Gln Met Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu		
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Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp		
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Val Cys Val Pro Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser		
885	890	895
Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val		
900	905	910

His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln  
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 Arg Thr Gly Lys Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys  
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 Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln  
 945 950 955 960  
 Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn  
 965 970 975  
 Gln Glu Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile  
 980 985 990  
 Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu  
 995 1000 1005  
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 1125 1130 1135  
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 1140 1145 1150  
 His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His  
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 Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala  
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Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn  
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Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln  
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Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu  
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Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile  
 1315 1320 1325

Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser  
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&lt;210&gt; 566

&lt;211&gt; 4047

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 566

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&lt;210&gt; 567

&lt;211&gt; 1199

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 567

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&lt;210&gt; 568

&lt;211&gt; 1199

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 568

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&lt;210&gt; 569

&lt;211&gt; 1199

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&lt;213&gt; Homo sapiens

&lt;400&gt; 569

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<211> 399

<212> PRT

<213> Homo sapiens

<400> 570

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His	Arg	Thr	Pro	Leu	Met	Lys	Ala	Leu	Gln	Cys	His	Gln	Glu	Ala	Cys	50	55	60
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Val	Val	Ala	Lys	Leu	Leu	Ser	His	Gly	Ala	Val	Ile	Glu	Val	His	Asn	100	105	110
Lys	Ala	Ser	Leu	Thr	Pro	Leu	Leu	Leu	Ser	Ile	Thr	Lys	Arg	Ser	Glu	115	120	125
Gln	Ile	Val	Glu	Phe	Leu	Leu	Ile	Lys	Asn	Ala	Asn	Ala	Asn	Ala	Val	130	135	140
Asn	Lys	Tyr	Lys	Cys	Thr	Ala	Leu	Met	Leu	Ala	Val	Cys	His	Gly	Ser	145	150	155
Ser	Glu	Ile	Val	Gly	Met	Leu	Leu	Gln	Gln	Asn	Val	Asp	Val	Phe	Ala	165	170	175
Ala	Asp	Ile	Cys	Gly	Val	Thr	Ala	Glu	His	Tyr	Ala	Val	Thr	Cys	Gly	180	185	190
Phe	His	His	Ile	His	Glu	Gln	Ile	Met	Glu	Tyr	Ile	Arg	Lys	Leu	Ser	195	200	205
Lys	Asn	His	Gln	Asn	Thr	Asn	Pro	Glu	Gly	Thr	Ser	Ala	Gly	Thr	Pro	210	215	220
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																		240

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 290 295 300  
 Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala Lys  
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 Glu Ile Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala  
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 Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro  
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 Glu His Tyr Ala Val Thr Cys Gly Phe His His Ile His Glu Gln Ile  
 35 40 45  
 Met Glu Tyr Ile Arg Lys Leu Ser Lys Asn His Gln Asn Thr Asn Pro  
 50 55 60  
 Glu Gly Thr Ser Ala Gly Thr Pro Asp Glu Ala Ala Pro Leu Ala Glu  
 65 70 75 80  
 Arg Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu  
 85 90 95  
 Ala Ala Pro Leu Val Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu Val  
 100 105 110

Glu Lys Thr Pro Asp Glu Ala Ala Ser Leu Val Glu Gly Thr Ser Asp  
 115 120 125  
 Lys Ile Gln Cys Leu Glu Lys Ala Thr Ser Gly Lys Phe Glu Gln Ser  
 130 135 140  
 Ala Glu Glu Thr Pro Arg Glu Ile Thr Ser Pro Ala Lys Glu Thr Ser  
 145 150 155 160  
 Glu Lys Phe Thr Trp Pro Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp  
 165 170 175  
 Glu Lys Lys Glu Asp Thr Pro Arg Glu Ile Met Ser Pro Ala Lys Glu  
 180 185 190  
 Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys Ile  
 195 200 205  
 Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala Arg  
 210 215 220  
 Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys Met  
 225 230 235 240  
 Ile Ala Cys Pro Thr Lys Glu  
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&lt;210&gt; 572

&lt;211&gt; 399

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 572

Thr Lys Arg Lys Lys Thr Ile Asn Leu Asn Ile Gln Asp Ala Gln Lys  
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 Arg Thr Ala Leu His Trp Ala Cys Val Asn Gly His Glu Glu Val Val  
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 Thr Phe Leu Val Asp Arg Lys Cys Gln Pro Asp Val Leu Asp Gly Glu  
 35 40 45  
 His Arg Thr Pro Leu Met Lys Ala Leu Gln Cys His Gln Glu Ala Cys  
 50 55 60  
 Ala Asn Ile Leu Ile Asp Ser Gly Ala Asp Ile Asn Leu Val Asp Val  
 65 70 75 80  
 Tyr Gly Asn Met Ala Leu His Tyr Ala Val Tyr Ser Glu Ile Leu Ser  
 85 90 95  
 Val Val Ala Lys Leu Leu Ser His Gly Ala Val Ile Glu Val His Asn  
 100 105 110  
 Lys Ala Ser Leu Thr Pro Leu Leu Leu Ser Ile Thr Lys Arg Ser Glu  
 115 120 125

Gln Ile Val Glu Phe Leu Leu Ile Lys Asn Ala Asn Ala Asn Ala Val  
 130 135 140  
 Asn Lys Tyr Lys Cys Thr Ala Leu Met Leu Ala Val Cys His Gly Leu  
 145 150 155 160  
 Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe Ala  
 165 170 175  
 Ala Asp Ile Cys Gly Val Thr Ala Glu His Tyr Ala Val Thr Cys Gly  
 180 185 190  
 Phe His His Ile His Glu Gln Ile Met Glu Tyr Ile Arg Lys Leu Ser  
 195 200 205  
 Lys Asn His Gln Asn Thr Asn Pro Glu Gly Thr Ser Ala Gly Thr Pro  
 210 215 220  
 Asp Glu Ala Ala Pro Leu Ala Glu Arg Thr Pro Asp Thr Ala Glu Ser  
 225 230 235 240  
 Leu Val Glu Lys Thr Pro Asp Glu Ala Ala Pro Leu Val Glu Arg Thr  
 245 250 255  
 Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu Ala Ala  
 260 265 270  
 Ser Leu Val Glu Gly Thr Ser Asp Lys Ile Gln Cys Leu Glu Lys Ala  
 275 280 285  
 Thr Ser Gly Lys Phe Glu Gln Ser Ala Glu Glu Thr Pro Arg Glu Ile  
 290 295 300  
 Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala Lys  
 305 310 315 320  
 Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Asp Thr Pro Arg  
 325 330 335  
 Glu Ile Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala  
 340 345 350  
 Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro  
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 Val Lys Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val  
 370 375 380  
 Leu Glu Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu  
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&lt;210&gt; 573

&lt;211&gt; 1349

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 573

Met Gln His His His His His His His Thr Lys Arg Lys Lys Thr Ile  
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Asn Leu Asn Ile Gln Asp Ala Gln Lys Arg Thr Ala Leu His Trp Ala  
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Cys Val Asn Gly His Glu Glu Val Val Thr Phe Leu Val Asp Arg Lys  
35 40 45

Cys Gln Pro Asp Val Leu Asp Gly Glu His Arg Thr Pro Leu Met Lys  
50 55 60

Ala Leu Gln Cys His Gln Glu Ala Cys Ala Asn Ile Leu Ile Asp Ser  
65 70 75 80

Gly Ala Asp Ile Asn Leu Val Asp Val Tyr Gly Asn Met Ala Leu His  
85 90 95

Tyr Ala Val Tyr Ser Glu Ile Leu Ser Val Val Ala Lys Leu Leu Ser  
100 105 110

His Gly Ala Val Ile Glu Val His Asn Lys Ala Ser Leu Thr Pro Leu  
115 120 125

Leu Leu Ser Ile Thr Lys Arg Ser Glu Gln Ile Val Glu Phe Leu Leu  
130 135 140

Ile Lys Asn Ala Asn Ala Asn Ala Val Asn Lys Tyr Lys Cys Thr Ala  
145 150 155 160

Leu Met Leu Ala Val Cys His Gly Leu Ser Glu Ile Val Gly Met Leu  
165 170 175

Leu Gln Gln Asn Val Asp Val Phe Ala Ala Asp Ile Cys Gly Val Thr  
180 185 190

Ala Glu His Tyr Ala Val Thr Cys Gly Phe His His Ile His Glu Gln  
195 200 205

Ile Met Glu Tyr Ile Arg Lys Leu Ser Lys Asn His Gln Asn Thr Asn  
210 215 220

Pro Glu Gly Thr Ser Ala Gly Thr Pro Asp Glu Ala Ala Pro Leu Ala  
225 230 235 240

Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp  
245 250 255

Glu Ala Ala Pro Leu Val Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu  
260 265 270

Val Glu Lys Thr Pro Asp Glu Ala Ala Ser Leu Val Glu Gly Thr Ser  
275 280 285

Asp Lys Ile Gln Cys Leu Glu Lys Ala Thr Ser Gly Lys Phe Glu Gln  
290 295 300

Ser Ala Glu Glu Thr Pro Arg Glu Ile Thr Ser Pro Ala Lys Glu Thr  
 305 310 315 320  
 Ser Glu Lys Phe Thr Trp Pro Ala Lys Gly Arg Pro Arg Lys Ile Ala  
 325 330 335  
 Trp Glu Lys Lys Glu Asp Thr Pro Arg Glu Ile Met Ser Pro Ala Lys  
 340 345 350  
 Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys  
 355 360 365  
 Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala  
 370 375 380  
 Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys  
 385 390 395 400  
 Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn  
 405 410 415  
 Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr  
 420 425 430  
 Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val  
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 Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu  
 450 455 460  
 Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu  
 465 470 475 480  
 Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln  
 485 490 495  
 Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp  
 500 505 510  
 Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser  
 515 520 525  
 Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp  
 530 535 540  
 Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu  
 545 550 555 560  
 Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu  
 565 570 575  
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 580 585 590  
 Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala  
 595 600 605  
 Leu Glu Leu Lys Asn Glu Gln Thr Trp Arg Ala Asp Glu Ile Leu Pro

610	615	620
Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Thr Glu		
625	630	635 640
Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala		
	645	650 655
Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser		
	660	665 670
Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser		
	675	680 685
Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala		
	690	695 700
Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln		
	705	710 715 720
Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu		
	725	730 735
Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu		
	740	745 750
Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys		
	755	760 765
Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp Lys Ile		
	770	775 780
Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ala		
	785	790 795 800
Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met		
	805	810 815
Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe		
	820	825 830
Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu		
	835	840 845
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu		
	850	855 860
Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu		
	865	870 875 880
Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His		
	885	890 895
Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser		
	900	905 910
Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu		
	915	920 925

Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met  
 930 935 940  
 Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu  
 945 950 955 960  
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 965 970 975  
 Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn  
 980 985 990  
 Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu  
 995 1000 1005  
 Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala  
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 Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn  
 1025 1030 1035 1040  
 Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn  
 1045 1050 1055  
 Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr  
 1060 1065 1070  
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 1075 1080 1085  
 Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu  
 1090 1095 1100  
 Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu  
 1105 1110 1115 1120  
 Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu  
 1125 1130 1135  
 Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro  
 1140 1145 1150  
 Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg  
 1155 1160 1165  
 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln  
 1170 1175 1180  
 Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val  
 1185 1190 1195 1200  
 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys  
 1205 1210 1215  
 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val  
 1220 1225 1230

Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys  
1235 1240 1245

Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His  
1250 1255 1260

Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser  
1265 1270 1275 1280

Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala  
1285 1290 1295

Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys  
1300 1305 1310

Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr  
1315 1320 1325

Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala  
1330 1335 1340

Glu Thr Glu Val Ile  
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cacacaaaga ggaagaagac catc

24

<210> 575  
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gattcttttg taggacatgc aatcatc

27

<210> 576  
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<213> Homo sapiens

<220>  
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&lt;223&gt; n = A,T,C or G

&lt;400&gt; 576

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<213> Homo sapiens

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Gln Thr Val Glu Phe Leu Leu Thr Lys Asn Ala Asn Ala Asn Ala Phe  
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Asn Glu Ser Lys Cys Thr Ala Leu Met Leu Ala Ile Cys Glu Gly Ser  
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Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe Ala  
65 70 75 80

Glu Asp Ile His Gly Ile Thr Ala Glu Arg Tyr Ala Ala Ala Arg Gly  
85 90 95

Val Asn Tyr Ile His Gln Gln Leu Leu Glu His Ile Arg Lys Leu Pro  
100 105 110

Lys Asn Pro Gln Asn Thr Asn Pro Glu Gly Thr Ser Thr Gly Thr Pro  
115 120 125

Asp Glu Ala Ala Pro Leu Ala Glu Arg Thr Pro Asp Thr Ala Glu Ser  
130 135 140

Leu Leu Glu Lys Thr Pro Asp Glu Ala Ala Arg Leu Val Glu Gly Thr  
145 150 155 160

Ser Ala Lys Ile Gln Cys Leu Gly Lys Ala Thr Ser Gly Lys Phe Glu  
165 170 175

Gln Ser Thr Glu Glu Thr Pro Arg Lys Ile Leu Arg Pro Thr Lys Glu  
180 185 190

Thr Ser Glu Lys Phe Ser Trp Pro Ala Lys Glu Arg Ser Arg Lys Ile  
195 200 205

Thr Trp Glu Glu Lys Glu Thr Ser Val Lys Thr Glu Cys Val Ala Gly  
210 215 220

Val	Thr	Pro	Asn	Lys	Thr	Glu	Val	Leu	Glu	Lys	Gly	Thr	Ser	Asn	Met
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 Thr Lys Ile Ile Ser Lys Ser Ala Ala Gln Asn Tyr Thr Cys Leu Pro  
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 305 310 315 320  
 Asp Gln Met Phe Pro Ser Glu Ser Lys Arg Glu Glu Asp Glu Glu Tyr  
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 Glu Ser Pro Asp Lys Asp Gly Leu Leu Lys Pro Thr Cys Gly Met Lys  
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 Ile Ser Leu Pro Asn Lys Ala Leu Glu Leu Lys Asp Arg Glu Thr Phe  
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 645 650 655  
 Lys Pro Thr Thr Glu Asn Ser Gln Ser Thr Lys Val Glu Glu Asp Phe  
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 Asn Leu Thr Thr Lys Glu Gly Ala Thr Lys Thr Val Thr Gly Gln Gln  
 675 680 685  
 Glu Arg Asp Ile Gly Ile Ile Glu Arg Ala Pro Gln Asp Gln Thr Asn  
 690 695 700  
 Lys Met Pro Thr Ser Glu Leu Gly Arg Lys Glu Asp Thr Lys Ser Thr  
 705 710 715 720  
 Ser Asp Ser Glu Ile Ile Ser Val Ser Asp Thr Gln Asn Tyr Glu Cys  
 725 730 735  
 Leu Pro Glu Ala Thr Tyr Gln Lys Glu Ile Lys Thr Thr Asn Gly Lys  
 740 745 750  
 Ile Glu Glu Ser Pro Glu Lys Pro Ser His Phe Glu Pro Ala Thr Glu  
 755 760 765  
 Met Gln Asn Ser Val Pro Asn Lys Gly Leu Glu Trp Lys Asn Lys Gln  
 770 775 780  
 Thr Leu Arg Ala Asp Ser Thr Thr Leu Ser Lys Ile Leu Asp Ala Leu  
 785 790 795 800  
 Pro Ser Cys Glu Arg Gly Arg Glu Leu Lys Lys Asp Asn Cys Glu Gln  
 805 810 815  
 Ile Thr Ala Lys Met Glu Gln Met Lys Asn Lys Phe Cys Val Leu Gln  
 820 825 830  
 Lys Glu Leu Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln  
 835 840 845  
 Lys Ala Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu Pro Leu Asn

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Arg Pro Glu Glu Gln Leu	Arg Lys Lys Leu Glu Val	Lys His Gln Leu
885	890	895
Glu Gln Thr Leu Arg Ile	Gln Asp Ile Glu Leu Lys	Ser Val Thr Ser
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Asn Leu Asn Gln Val Ser	His Thr His Glu Ser Glu	Asn Asp Leu Phe
915	920	925
His Glu Asn Cys Met Leu	Lys Lys Glu Ile Ala Met	Leu Lys Leu Glu
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Val Ala Thr Leu Lys His	Gln His Gln Val Lys Glu	Asn Lys Tyr Phe
945	950	955 960
Glu Asp Ile Lys Ile Leu	Gln Glu Lys Asn Ala Glu	Leu Gln Met Thr
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Leu Lys Leu Lys Gln Lys	Thr Val Thr Lys Arg Ala	Ser Gln Tyr Arg
980	985	990
Glu Gln Leu Lys Val Leu	Thr Ala Glu Asn Thr Met	Leu Thr Ser Lys
995	1000	1005
Leu Lys Glu Lys Gln Asp	Lys Glu Ile Leu Glu Thr	Glu Ile Glu Ser
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His His Pro Arg Leu Ala	Ser Ala Leu Gln Asp His	Asp Gln Ser Val
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Thr Ser Arg Lys Asn Gln	Glu Leu Ala Phe His Ser	Ala Gly Asp Ala
1045	1050	1055
Pro Leu Gln Gly Ile Met	Asn Val Asp Val Ser Asn	Thr Ile Tyr Asn
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Asn Glu Val Leu His Gln	Pro Leu Tyr Glu Ala Gln	Arg Lys Ser Lys
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Ser Pro Lys Ile Asn Leu	Asn Tyr Ala Gly Asp Asp	Leu Arg Glu Asn
1090	1095	1100
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Gln Met Lys Lys Ala Glu	His Met Tyr Gln Asn Glu	Gln Asp Asn Val
1125	1130	1135
Asp Lys His Thr Glu Gln	Gln Glu Ser Leu Glu Gln	Lys Leu Phe Gln
1140	1145	1150
Leu Glu Ser Lys Asn Arg	Trp Leu Arg Gln Gln Leu	Val Tyr Ala His
1155	1160	1165

Lys Lys Val Asn Lys Ser Lys Val Thr Ile Asn Ile Gln Phe Pro Glu  
 1170 1175 1180

Met Lys Met Gln Arg His Leu Lys Glu Lys Asn Glu Glu Val Phe Asn  
 1185 1190 1195 1200

Tyr Gly Asn His Leu Lys Glu Arg Ile Asp Gln Tyr Glu Lys Glu Lys  
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Ala Glu Arg Glu Val Ser Ile Lys Lys Tyr Lys Tyr Phe Ser Asn Phe  
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Leu Lys Glu Ser Gly Leu Gly  
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 <212> PRT  
 <213> Homo sapiens

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 Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile  
 5 10 15

Tyr Gln Tyr Glu  
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<210> 579  
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 <212> PRT  
 <213> Homo sapiens

<400> 579  
 Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp  
 5 10 15

Gln Lys Leu Phe  
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<210> 580  
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 <212> PRT  
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<400> 580  
 Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser  
 5 10 15

Lys Asn Met Trp  
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Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu  
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Lys Val Leu Ile  
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Ser Thr Ile Tyr  
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<400> 583  
Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val  
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Leu His Gln Pro  
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<210> 584  
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<400> 584  
Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn  
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Glu Asn Tyr Leu  
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<210> 585  
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<212> PRT  
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<400> 585

Glu Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn  
5 10 15

Cys Met Leu Lys  
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<210> 586

<211> 20

<212> PRT

<213> Homo sapiens

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Glu Asn Tyr Leu Leu His Glu Asn Leu Met Leu Lys Lys Glu Ile Ala  
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Met Leu Lys Leu  
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<210> 587

<211> 21

<212> PRT

<213> Homo sapiens

<400> 587

Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala  
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Thr Leu Lys His Gln  
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<210> 588

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<212> PRT

<213> Homo sapiens

<400> 588

Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu  
5 10 15

Ala Glu Ile Glu  
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<210> 589

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<212> PRT

<213> Homo sapiens

<400> 589

Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro  
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Arg Leu Ala Ser  
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<400> 590  
Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp  
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His Asp Gln Ile  
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<210> 591  
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<400> 591  
Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg  
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Lys Ser Gln Glu  
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<400> 592  
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Ile Ala Gly Asp  
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<213> Homo sapiens

<400> 593  
Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln  
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Arg Lys Met Asn  
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<210> 594  
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Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn  
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Glu Asn Tyr Leu  
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<210> 595  
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Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met  
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Leu Lys Lys Glu  
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Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu  
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Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln  
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Glu Lys Glu Asn  
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<210> 598  
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Lys Ile Leu Lys  
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Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln  
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Asp Lys Glu Ile  
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<400> 604  
Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu  
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Ser His His Pro  
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<210> 605  
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<400> 605  
Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val  
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Gln Asp His Asp  
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<400> 606  
Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg  
1 5 10 15  
Lys Ser Gln Glu  
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<400> 608  
Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn  
1 5 10 15  
Val Asp Val Ser  
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<210> 609  
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<212> PRT  
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Glu Val Leu His  
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<210> 610  
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Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala  
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Gln Arg Lys Ser  
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<210> 611  
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<400> 611  
His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile  
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Asn Leu Asn Tyr Ala  
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<210> 612  
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<400> 612  
Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu  
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Asn Thr Leu Val  
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<210> 613  
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1 5 10 15

Asp Gln Arg Glu  
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<210> 614  
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<400> 614  
Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys  
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Glu Ala Glu His  
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<210> 615  
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<400> 615  
Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn Glu Gln  
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Asp Asn Val Asn  
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<210> 616  
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<400> 616  
Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln  
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Glu Ser Leu Asp  
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<210> 617  
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<400> 617  
Lys His Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu  
1 5 10 15  
Gln Ser Lys Asn  
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<210> 618  
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<212> PRT  
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<400> 618  
Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln

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1 5 10 15  
Gln Leu Val His Ala  
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<210> 619  
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<212> PRT  
<213> Homo sapiens

<400> 619  
Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn  
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Lys Ser Lys Ile  
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<210> 620  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 620  
His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe  
1 5 10 15  
Leu Glu Arg Lys  
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<210> 621  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 621  
Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu  
1 5 10 15  
Lys Glu Lys Asn  
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<210> 622  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 622  
Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr  
1 5 10 15  
Asn Asn His Leu  
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<210> 623  
<211> 20  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 623

Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln  
 1 5 10 15  
 Tyr Glu Lys Glu  
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&lt;210&gt; 624

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 624

Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu  
 1 5 10 15  
 Thr Glu Val Ile  
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&lt;210&gt; 625

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 625

Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu  
 1 5 10 15  
 Asn Glu Lys Ile Arg Glu Glu Leu Gly Cys Gly  
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&lt;210&gt; 626

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 626

Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu  
 1 5 10 15  
 Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Gly Cys Gly  
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&lt;210&gt; 627

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 627

Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu  
 1 5 10 15  
 Ser Asn Leu Asn Gln Gly Cys Gly  
 20

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/12378

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; A01N 43/04; C07K 14/00; C07H 21/04  
US CL : 435/6, 325, 375; 514/44; 530/350; 536/23.1, 24.5

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
U.S. : 435/6, 325, 375; 514/44; 530/350; 536/23.1, 24.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
Please See Continuation Sheet

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 00/43420 A1 (ABBOTT LABORATORIES) 27 July 2000 (27.07.2000), see Figure 1.	1-12



Further documents are listed in the continuation of Box C.



See patent family annex.

\* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

11 July 2002 (11.07.2002)

Date of mailing of the international search report

Authorized officer

Janet L. Epps, Ph.D.

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

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Washington, D.C. 20231

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Telephone No. 703-308-0196

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/12378

**Continuation of B. FIELDS SEARCHED Item 3:**  
CaPlus, Medline, Biosis, USPAT, EPO, JPO, Derwent  
search terms: breast specific polypeptide, sequence search of SEQ ID NO: 537-547